

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2001, 07:16:03 ; Search time 885.31 seconds
(without alignments)
2010.484 Million cell updates/sec

Title: US-09-199-129A-1
Perfect score: 254
Sequence: 1 ggaatcgaagcaccctta.....atgaacaaagcttcagaca 254

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7991742 seqs, 3503743858 residues
1 number of hits satisfying chosen parameters: 15983484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est25:*
26: gb_est26:*
27: gb_est27:*
28: gb_est28:*
29: gb_est29:*
30: gb_est30:*
31: gb_est31:*
32: gb_est32:*
33: gb_est33:*
34: gb_est34:*
35: gb_est35:*
36: gb_est36:*
37: gb_est37:*
38: gb_est38:*
39: gb_est39:*
40: gb_est40:*
41: em_estba:*
42: em_estfun:*
43: em_esthum1:*

44: em_esthum2:*
45: em_esthum3:*
46: em_esthum4:*
47: em_esthum5:*
48: em_esthum6:*
49: em_esthum7:*
50: em_esthum8:*
51: em_esthum9:*
52: em_esthum10:*
53: em_esthum11:*
54: em_esthum12:*
55: em_esthum13:*
56: em_esthum14:*
57: em_esthum15:*
58: em_esthum16:*
59: em_esthum17:*
60: em_esthum18:*
61: em_esthum19:*
62: em_esthum20:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estov1:*
68: em_estov2:*
69: em_estp11:*
70: em_estp12:*
71: em_estp13:*
72: em_estp14:*
73: em_estp15:*
74: em_estro1:*
75: em_estro2:*
76: em_estro3:*
77: em_estro4:*
78: em_estro5:*
79: em_estro6:*
80: em_estro7:*
81: em_estro8:*
82: em_estro9:*
83: em_estro10:*
84: em_estro11:*
85: em_estro12:*
86: em_estro13:*
87: gb_est41:*
88: gb_est42:*
89: gb_est43:*
90: gb_est44:*
91: gb_est45:*
92: gb_est46:*
93: gb_est47:*
94: gb_est48:*
95: gb_est49:*
96: gb_est50:*
97: gb_est51:*
98: gb_est52:*
99: gb_est53:*
100: gb_est54:*
101: gb_est55:*
102: gb_est56:*
103: gb_est57:*
104: gb_est67:*
105: gb_est68:*
106: gb_est69:*
107: gb_est70:*
108: gb_est71:*
109: gb_est72:*
110: gb_est73:*
111: gb_est74:*
112: em_esthum21:*
113: em_esthum22:*
114: em_esthum23:*
115: em_estom1:*
116: em_estom2:*

117: em_estp16:*
 118: em_estp17:*
 119: em_estp18:*
 120: em_estp19:*
 121: em_estp20:*
 122: em_estp21:*
 123: em_estp22:*
 124: em_estp23:*
 125: em_estp24:*
 126: em_estp25:*
 127: em_estp26:*
 128: em_estp27:*
 129: em_estp28:*
 130: em_estp29:*
 131: em_estp30:*
 132: em_estp31:*
 133: em_estp32:*
 134: em_estp33:*
 135: em_estp34:*
 136: em_estp35:*
 137: em_estp36:*
 138: em_estp37:*
 139: em_estp38:*
 140: em_estp39:*
 141: em_estp40:*
 142: em_estp41:*
 143: em_estp42:*
 144: em_estp43:*
 145: em_estp44:*
 146: em_estp45:*
 147: em_estp46:*
 148: em_estp47:*
 149: em_estp48:*
 150: em_estp49:*
 151: em_estp50:*
 152: em_estp51:*
 153: em_estp52:*
 154: em_estp53:*
 155: em_estp54:*
 156: em_estp55:*
 157: em_estp56:*
 158: em_estp57:*
 159: em_estp58:*
 160: em_estp59:*
 161: em_estp60:*
 162: em_estp61:*
 163: em_estp62:*
 164: em_estp63:*
 165: em_estp64:*
 166: em_estp65:*
 167: em_estp66:*
 168: em_estp67:*
 169: em_estp68:*
 170: em_estp69:*
 171: em_estp70:*
 172: em_estp71:*
 173: em_estp72:*
 174: em_estp73:*
 175: em_estp74:*
 176: em_estp75:*
 177: em_estp76:*
 178: em_estp77:*
 179: em_estp78:*
 180: em_estp79:*
 181: em_estp80:*
 182: em_estp81:*
 183: em_estp82:*
 184: em_estp83:*
 185: em_estp84:*
 186: em_estp85:*
 187: em_estp86:*
 188: em_estp87:*
 189: em_estp88:*

190: gb_gss25:*
 191: gb_gss26:*
 192: gb_gss27:*
 193: gb_gss28:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	127.6	50.2	477	28	AL369727	AL369727 MCB32H11
2	127.6	50.2	604	105	BE204104	BE204104 EST396780
3	127.6	50.2	628	105	BE204201	BE204201 EST396877
4	119.4	47.0	948	94	AM722203	AM722203 GA_Ea001
5	110.4	43.5	463	108	BE462089	BE462089 EST34351
6	110.4	43.5	468	137	BE921143	BE921143 EST424912
7	108.8	42.8	263	39	AM041721	AM041721 EST284585
8	108.8	42.8	608	108	BE449253	BE449253 EST356108
9	107.8	42.4	529	97	AM934135	AM934135 EST359978
10	107.8	42.4	807	108	BE420773	BE420773 HMM002.D0
11	104.6	41.2	714	105	BE193174	BE193174 HVMEM008
12	103.4	40.7	547	110	BE598903	BE598903 P11_83_A0
13	102.8	40.5	290	28	AT002063	AT002063 AT002063
14	102.8	40.5	411	28	AT001761	AT001761 AT001761
15	99.6	39.2	564	93	AM624478	AM624478 EST322423
16	99.2	39.1	646	106	BE320109	BE320109 NF025B04R
17	99.2	39.1	699	92	AM584510	AM584510 N210564e
18	98.6	38.8	509	92	AM560421	AM560421 EST315469
19	96.4	38.0	417	26	A1898214	A1898214 EST267657
20	94.6	37.2	380	144	R65185	R65185 13689 Lambd
21	94.2	37.1	191	108	BE459125	BE459125 EST414417
22	94	37.0	555	27	A1993867	A1993867 701515234
23	82.4	32.4	474	29	A0084980	A0084980 A0084980
24	80.6	31.7	494	94	AM754529	AM754529 PC03C03 P
25	78.6	30.9	584	190	AG033012	AG033012 Oryza sat
26	77.2	30.4	337	111	BE662436	BE662436 ST85/ST85
27	77.2	30.4	344	87	AM226329	AM226329 ST81B04 P
28	77.2	30.4	351	90	AM437935	AM437935 ST78E07 P
29	77.2	30.4	380	87	AM226271	AM226271 ST80D09 P
30	77.2	30.4	389	39	AM056809	AM056809 ST56D12 P
31	77.2	30.4	390	39	AM056655	AM056655 ST54C03 P
32	77.2	30.4	460	92	AM587778	AM587778 ST66G08 P
33	77.2	30.4	469	24	A1726703	A1726703 BNGH1637
34	77.2	30.4	573	39	AM042658	AM042658 ST73A07 P
35	77.2	30.4	601	39	AM043146	AM043146 ST79H08 P
36	77.2	30.4	700	93	AM043255	AM043255 ST1B10 P
37	77.2	30.4	775	38	AM668560	AM668560 GA_Ea001
38	77.2	30.4	889	94	AM010325	AM010325 ST04G01 P
39	77.2	30.4	889	94	AM731435	AM731435 GA_Ea003
40	77.2	30.4	973	94	AM731454	AM731454 GA_Ea003
41	76.2	30.0	250	109	BE529534	BE529534 M74H09STM
42	76.2	30.0	384	37	AV551838	AV551838 AV551838
43	76.2	30.0	549	39	AM042889	AM042889 ST26F06 P
44	76.2	30.0	565	37	AV550681	AV550681 AV550681
45	76.2	30.0	568	37	AV549801	AV549801 AV549801

ALIGNMENTS

RESULT 1
 AL369727 AL369727 477 bp mRNA
 LOCUS MCB32H11F1 MCB32H11F1 477 bp mRNA
 DEFINITION MCB32H11F1 MCB32H11F1 MCB32H11F1 MCB32H11F1 MCB32H11F1
 ACCESSION AL369727
 VERSION AL369727.1 GI:9669480
 KEYWORDS EST.
 SOURCE barrel medic.

	ORGANISM	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta Magnoliophyta; eudicotyledons: core eudicots: Rosidae; eurosids I; Fabales: Fabeaceae: Papilionoideae; Medicago.
REFERENCE	AUTHORS	Journet,E.P., Crespeau,H., van-Tuijnem,D., Guzy,J., Jailion,O., Michel,A., Carreau,V., Chataigner,O., Kahn,D., Gianinazzi-Pearson ,V. and Gamas,P.
TITLE	Medicago truncatula ESTs from nitrogen-starved roots	
JOURNAL	Unpublished (200)	
COMMENT	Genoscope - Centre National de Sequencage BP 191 91006 Evry cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de Biologie Moleculaire des Relations Plantes-Microorganismes, CNRS-IRRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@toulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).	
FEATURES	source	/organism="Medicago truncatula" /cultivar="Jemalong" /db_xref="taxon:3880" /clone_"MtbA32H1I" /_clone_11b-"MCBA" /_tissue_type_"root tips" /_dev_stage_"harvested after 3 days of N-starvation" /note_"vector: pbluescript psk; Site1.: ECOR1; Site 2: XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from poly(A)-enriched RNA. The cDNA was directionally ligated into Uni-zapXR vector from Stratagene and packaged using GibcoPack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using Exasit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequenceage (Genoscope, Evry, France)." .
BASE COUNT	140 a 85 c 95 g 157 t	
ORIGIN		
Query Match	Best Local Similarity 50.2%; Score 127.6; DB 28; Length 477;	
Matches 148:	Conservative 0; Mismatches 40; Indels 0; Gaps 0;	
Df	67 ctactgacctcttcctcnaactcgacactcatcgtgcgtgaattttctcgaaga 126 98 CTTCTTTCCTTAATACACTTTCAATTGCTGAAGATAATTTGGAAAGA 157	
Oy	127 gatctgaagtatgatggaaaggccnlttggtctancagattggaaaagdtgaaga 186 Db 158 CATTCAGAGTGCGGAAGACGTCTGGCCTTTATTCGATTGCAAAACAAGTAGA 217	
Oy	187 aaegcgtaaccctcaaacacacagacaagaanaatgtcltggagatcnagacnaagtc 246 Db 218 AAGCAGGTRACCTTTAAGTACTGCTGGAAAAATGGCCCTCATATCTGATGACAAAGTA 277	
Oy	247 ttcacaga 254 	
Db	278 TTCAGACA 285	
RESULT	2	
LOCUS	BE204104 604 bp mRNA EFT -05-SEP-2000	
DEFINITION	EST396780 KVO Medicago truncatula cDNA clone pkV0-14B21, mRNA sequence.	
ACCESION	BE204104	
VERSION	BE204104.1 GI:8747387	
KEYWORDS	EST.	

SOURCE		barrel medic.
ORGANISM		Medicago truncatula Eubryotia; Viridiplantae; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago. 1 (bases 1 to 604)
REFERENCE		Vandenbosch,K., Endre,G., Hur,J.J., Moore,J., Beremand,P., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
TITLE		Estrs from uninoculated seedling roots of Medicago truncatula
JOURNAL		Unpublished (1999)
COMMENT		Contact: Vandenbosch K Department of Biology Texas A&M University College Station, TX 77843-3258, USA Tel.: 409 845 7707 Fax: 409 845 2891 Email: kate@mail.bio.tamu.edu Texas A&M University name: t263876e TIGR sequence name: MTGAO11yr More information is available at: http://chr.sysie.tamu.edu/mcdicoag Seq primer: SKmod (CTA gaa cta gcg gat cc). Location/Qualifiers 1..604 /organism="Medicago truncatula" /cultivar="genotype Al7" /db_xref="taxon:3880" /cloned="pkv0-14B21" /clone_11b-"KV0" /tissue_type="Seedling roots" /dev_stage="Immediately prior to inoculation with Sinorhizobium meliloti (0 hour)" /lab_host="E.coli strain XL0LR" /note="Vector: pBluescript SK -; Site_1: EcoRI; Site_2: XhoI; CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the UniZap XR vector from strata gene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cdna inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."
BASE COUNT	178 a 105 c 130 g 191 t	
ORIGIN		
Query Match	50.2%	Score 127.6; DB 105; Length 604;
Best Local Similarity	78.7%;	Pred. No. 4.3e-29;
Matches 148:	Conservative 0; Mismatches 40; Indels 0; Gaps 0;	
OY	67 ctactgncttcttcctaactcgcacgtccatcgcatcgtagattttctctgaaga	126
Dd		
Dd	13 CTCCTTTCCCTTCATATAACACTTTTCATTTCTTCATTGGCTAGATATTTTTGCAAGACA	72
OY	127 gattcgaagaatgatgatgaagaagcgcnltgggtgclanccgatctgaagaaggatgaaggaa	186
Dd		
Dd	73 CATTCAGAAGATGGGGGAAAGACTCGTGCGGTTCATTCGATTGCGAAGAAGCATGAAGACA	132
OY	187 aaagcggctaccttcaagcacacagcagaagaaaatggctcggggatccngatgcanaagtgc	246
Dd		
OY	133 AAGCAGGTAACCCTTTAAGTATATCTCTGGAAAAATGGCTCGATCATCTGATGACAAAGCTA	192
Dd		
OY	247 ttcaaaca 254	
Dd		
Dd	193 TTCAAGACA 200	
RESULT	3	
BE204201	628 bp	mRNA EST 05-SEP-2000
LOCUS	EST3396877	KV0 Medicago truncatula cDNA clone pkv0-14F14, mRNA
DEFINITION	sequence.	
ACCESION	BE204201	
VERSION	BE204201.1	GI:8747485

Query Match	42.8%	Score 108.8	DB 39	Length 263
Best Local Similarity	70.7%	Pred. No. 2.3e-23		
Matches 140:	Conservative	0	Mismatches 58	Indels 0
			Gaps	0
Db	11	AVCAATTTCTACTAAATTTGGTTACTATATTCGCAATTAATACATGCATATTAATCGAGATCCT	70	
56	atcgcctcaagctactgcttcccttcctcnaactctgcactcttcacttcgcgtgatttt	115		
116	cttcgaaagaagactcgaagaatgagatggaaagccggnigggtccancgcattggaagaag	175		
71	CTTTGAGAGACAAATTTGATGATGATTTGGACAGACAGATGGCGAAGACTGATCGTGAAGAAG	130		
176	gagtgaaagaaagcgggttaccttcaagcacacacagagaagaatggtctgggacatcnga	235		
131	GAGTGAAGGAAAGGAGAGCGCTCTTAAGCATACACTGCGCAATATGGCTGTGATCTCTGA	190		
236	tgacnaaggtcttcagac	253		
191	TGATTAAGGTATTCATAC	208		
RESULT 8				
BE449253	608 bp	mRNA	EST	26-JUL-2000
LOCUS	EST356108	L. hirsutum trichome, Cornell University	Lycopersicon	
DEFINITION	hirsutum cDNA clone cLHT31A6, mRNA sequence.			
ACCESSION	BE449253			
VERSION	BE449253.1	GI:9454852		
KEYWORDS	EST.			
SOURCE	Lycopersicon hirsutum.			
ORGANISM	Lycopersicon hirsutum.			
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum; Lycopersicon.			
AUTHORS	van der Hoeven,R.S., Bezzeredes,J.L., Matern,A.L., Holt,I.E., Liang,F., Hansen,T., Craven,M.B., Bowman,C.L., Ronning,C.M., Nierman,W., Friser,C.M., Matlin,G.B., Giovannoni,J.J. and Tanksley,S.D.			
TITLE	Generation of ESTs from wild tomato (Lycopersicon hirsutum) trichomes			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: David Frisch Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29654, USA Tel: 864 656 4366 Fax: 864 656 4393 Email: dfrisch@CLEMSON.EDU			
FEATURES	5 prime sequence.			
SOURCE	Location/Qualifiers			
	1..608			
	/organism="Lycopersicon hirsutum"			
	/db_xref="taxon:62890"			
	/clone="cLHT31A6"			
	/clone_lib="L. hirsutum trichome, Cornell University"			
	/tissue_type="trichome"			
	/dev_stage="mixed stages"			

BASE COUNT	188 a	113 c	135 g	172 t
ORIGIN				
Query Match				
Best Local Similarity	70.7%	Pred. No. 2.9e-23;		
Matches 140;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;
OY	56 atcgcgttaagctactctgcttcttccttccttcnaactctgcacctcttcacgttcgcttgagattt	115		
DB	26 ATCATTTCTACTAGTTTGTCTACTCTGTTTTCATATAATTAACATCTTCATTTTCTGAGATCTT	85		
OY	116 ctctcaagaagagactcgaagaatgagatggaaagaccgmggggtgctcancgacttgaaag	175		
DB	86 CTTTAAACAACATTTGATGTGATGATGGCAGAGCAGATGGGTGAAGTGTGACTGGAAAG	145		
OY	176 gagtgaagaaagcgggtaccttcctaagcacacagcagaaatggtctgggataccnga	235		
DB	146 GAGTGAAGGAAGAAAGCAGGCTCTTAAACCATATACACTGGGAATAGGCTGGTACTCTGA	205		
OY	236 tgacnaaggtcttcagac	253		
DB	206 TGATTAAGCTATTCAGAC	223		
RESULT 9				
LOCUS	AM934135	529 bp	mRNA	EST
DEFINITION	EST359978 tomato fruit mature green, TAMU Lycopersicon esculentum			30-MAY-2000
ACCESSION	AM934135			
VERSION	AM934135.1	GI:8109536		
KEYWORDS	EST.			
SOURCE	tomato.			
ORGANISM	Lycopersicon esculentum			
REFERENCE	Eukaryotes: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots: Asteridae: euasterids I: Solanales: Solanaceae; Solanum: Lycopersicon.			
AUTHORS	I (bases 1 to 529) Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F., Upson,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Romling,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.			
TITLE	Generation of ESTs from tomato fruit tissue			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: David Frisch Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 4366 Fax: 864 656 4293 Email: dfrisch@CLEMSON.EDU			
FEATURES	5 prime sequence.			
source	Location/Qualifiers 1..529 /organism="Lycopersicon esculentum" /cultivar="T496" /db_xref="taxon:4081" /clone="CLEF57P10" /clone_1db="tomato fruit mature green, TAMU" /tissue_type="fruit pericarp" /dev_stage="mature green (3-5 days pre-ripening)" /lab_host="SOLR" /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; CLEF - Fruit were tagged at the 1cm stage and harvested 3-5 days prior to ripening. Fruit were cut in half to verify the seeds were indeed 'immature' and the seeds and locules were discarded prior to freezing the pericarp"			

ORIGIN	BASE COUNT	165 a	96 c	119 g	149 t
Query Match	42.4%	Score 107.8:	DB 97:	Length 529:	
Best Local Similarity	75.6%:	Pred. No. 5.7e-23:			
Matches 130:	Conservative 0:	Mismatches 42:	Indels 0:	Gaps 0:	
Oy	82	ttcnaacctctgacaccttcattccttcgcttgagatlttcttcgaagaagatcgcgaagatgat 141			
Db	52	ttttcaattatattatcaattcttcattatattctgaagatcttctttgaaacacaaatttgatgaatttt 111			
Oy	142	ggaagaagccgntgggctgcancagcatttggaaagaagatgaagaagaagccggttacctca 201			
Db	112	ggcacaagcagatgcgctgaagctgactgcaaaagcagtaaacggaagcagcagctcctttta 171			
Oy	202	agcacacagcaggaagaatgctctgggagatcgcagatgacnaaggtcttcagac 253			
Db	172	agcattacagctgggaattggcctgctgatctgatgattaaagattttcagac 223			
LOCUS	BE420773				
DEFINITION	BE420773 807 bp mRNA	EST	24-JUL-2000		
ACCESSION	HM0002.D06	ITEC HMM Barley Leaf Library	Hordeum vulgare	CDNA clone	
VERSION	BE420773				
KEYWORDS	BE420773.1	GI:9416616			
SOURCE	EST.				
ORGANISM	Hordeum vulgare				
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta				
AUTHORS	Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.				
	1 (bases 1 to 807)				
	Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier				
	,S., Dubcovsky,D., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,				
	Herrmann,R.G., Holton,T., Jacquemart,J.M., Jia,J., Joudrier,P.,				
	Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,				
	Pechion,L.N., Qualset,C., Schuch,W., Selvaraj,C., Shariflou,M.,				
	Sorrells,M., Warburton,M., and Wenzel,G.				
	International Triticeae EST Cooperative (ITEC): Production of				
	Expressed Sequence Tags for Species of the Triticeae				
	Unpublished (2000)				
JOURNAL	Contact: Herrmann RG				
COMMENT	Botanisches Institut der LMU				
	Menzinger Str. 67, D-80638 Munchen GERMANY				
	Fax: 49 30 171683				
	Email: herrmann@botanik.biologie.uni-muenchen.de				
	International Triticeae EST Cooperative (ITEC)				
	http://wheat.pw.usda.gov/genome.				
FEATURES	Location/Qualifiers				
SOURCE	1..807				
	/organism="Hordeum vulgare"				
	/cultivar="Barke"				
	/db_xref="taxon:4513"				
	/clone="HM0002.D06"				
	/clone_lib="ITEC HMM Barley Leaf Library"				
	/tissue_type="leaf"				
	/dev_stage="14 day old"				
	/note="Vector: pBluescriptSK(-); 850 bp average insert				
	size."				
BASE COUNT	210 a	206 c	215 g	170 t	6 others
ORIGIN					
Query Match	42.4%	Score 107.8:	DB 108:	Length 807:	
Best Local Similarity	80.0%:	Pred. No. 6.4e-23:			
Matches 124:	Conservative 0:	Mismatches 31:	Indels 0:	Gaps 0:	
Oy	100	cattgcctgagatcttcttcctcgaagaagatcgaagaatgagcgaagccgntggctgc 159			
Db	248	cctccggggaggtatcttccagagacgcttcgaagaatggttggaagacacgttgagta 307			

Oy	160	tancgattctggaaaagsgtgaaggaaacgcgggtacccttcagaacacagcaggaataat	219
Dd	308	AATCCGATTGGAAAAAGCGACGAAGAACC GGTTACTTTCACGCACA GCGCAGGAAAT	367
OY	220	ggtctgggatccngatcgacaagaagtcttcagaca	254
Dd	368	ATTCTGGGATCTTGATGTACAAAAGCATTTCAACACA	402


```

RESULT      11
BEI93174    mRNA          EST           25-JUL-2000
LOCUS       BEI93174
DEFINITION  HVSMEN008OA07f Hordeum vulgare 5-45 DAP spike EST library
            HVCNMA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMen008OA07f
SOURCE      mRNA sequence.
VERSION     BEI93174
KEYWORDS    GI:8705353
ORGANISM   barley
            Hordeum vulgare
Eukaryote; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliopsida; Liliopsida; Poales; Poaceae; Hordeum.
1 (bases 1 to 714)
Wing R., Close T.J., Kleinhofs A., Wise R., Begum D., Frisch D., Yoo S.-M.,
Anderson H., Dale J.E., Henry D., Kermode S., Palmer M., Rambo J.L., Sakai C., Schwartzbeck J., Simmons J., Choi D.W., Main D. and Wood P.
Development of a genetically and physically anchored EST resource for barley genomics
Unpublished (2000)
Contact: Wing RA
             Clemson University Genomics Institute
             Clemson University
             100 Jordan Hall, Clemson, SC 29634, USA
             Tel.: 864 656 7288
             Fax: 864 656 4293
             Email: rwing@clemson.edu
Seq primer: ATTTAACCTCTACTTAAGG
High quality sequence start: 187
High quality sequence stop: 454.
Location/Qualifiers
1..714
 /organism="Hordeum vulgare"
 /cultivar="Morex"
 /db_xref="taxon:4513"
 /clone="HVSMEn008OA07f"
 /clone="HVSMEn008OA07f"
 /clone.lib="Hordeum vulgare 5-45 DAP spike EST library
HVCNMA0009 (5 to 45 DAP)"
 /rname_type="5-45 DAP Spike"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT      192 a      188 c      183 g      150 t      1 others
ORIGIN
Query Match      41.2%; Score 104.6; DB 105; Length 714;
Best Local Similarity 78.7%; Pred. No. 6.1e+22;
Matches 122; Conservative 0; Mismatches 33; Indels 0; Gaps 0.
```

OY	100	cattgccgaatatcttccttgcaagagatcgaaagatgcatgtagaagacgnitgggtgc	159
Dd	123	CCTCCGGGGAGTCTCTTCGANAGCGGTTTCGAAGATGTGGGAGACACCTTGCTCA	182
OY	160	tanccgatttgtaaaaagsgtgaaggaaacgcgggtacccttcagaacacagcaggaataat	219
Dd	183	AATCCGATTGGAAAAAGCGACGAAGAACC GGTTACTTTCACGCACA GCGCAGGAAAT	242
OY	220	ggtctgggatccngatcgacaagaagtcttcagaca	254
Dd	243	ATTCTGGGATCTTGATGTACAAAAGCATTTCAACACA	277

RESULT 12

BE598903
LOCUS BE598903 547 bp mRNA EST 18-AUG-2000
DEFINITION P11_83_A08.b1_A002 Pathogen induced 1 (P11) Sorghum bicolor cDNA, mRNA sequence.
ACCESSION BE598903
VERSION BE598903.1 GI:9653962
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sorghum.
1 (bases 1 to 547)
Cordonnier-Pratt,M.-M., Gingle,A., Dean,R., Sudman,M. and Pratt,L.H.
REFERENCE An EST database from Sorghum: pathogen-induced plants
AUTHORS Unpublished (2000)
JOURNAL Contact: Cordonnier-Pratt MM
COMMENT Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: empratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: JEN REV
High quality sequence stop: 478
POLY-A-No.

FEATURES
source Location/Qualifiers
1..547
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_id="Pathogen induced 1 (P11)"
/note="Organ: Anthracnose induced 48 hr after inoculation:
two-week-old sorghum plants 48 hr after inoculation:
Vector: pBluescript II from lambda zap II; Site 1: XhoI;
Site 2: EcoRI; Two-week-old sorghum plants (BTX 623
cultivar) were infected with pathogen (isolate FRM421 of
Colletotrichum graminicola, which is a sorghum isolate).
RNA was prepared from infected leaves harvested from 45
seedlings 48 hours after inoculation. Note: young
seedlings (2 weeks old) exhibit juvenile resistant
reaction, which is an incompatible interaction. As they
grow older (4 weeks or older), plants resume susceptibility
to anthracnose disease. The library was made from poly-A
RNA in the cloning vector lambda zap II. Clones to be
sequenced were prepared by mass excision. WARNING: While
most or all ESTs are expected to derive from the host
plant, no effort was made to eliminate ESTs deriving from
the pathogen."

BASE COUNT 136 a 142 c 142 g 127 t
ORIGIN

Query Match 40.7%; Score 103.4; DB 110; Length 547;
Best Local Similarity 75.8%; Pred. No. 1.3e-21;
Matches 125; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

OY 90 ctgaccccttcattcgcctgagatttcttcgaagagatcgaagatgagatgaagagc 149
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 116 CTGCTCCCTCGCTTCGCGTGAATGCTCTTCAGAGAGCGCTTCGAGAGTGGAGAGT 175
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 150 cgnctgggtctancagattgtaaaagagatgaagaaagcgggtactctcaagacaca 209
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 176 CGGTGGGAGATGCGATTCGATTAAGAAAGAGTGAAGGAAAGCTGGAAGTTCAACACACA 235
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 210 gcagagaaaaatggtctgggagatcngatgaacaaaggtcttcagaca 254
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 236 GCGGGGAGATCTCTGCAATCTGATGACAAAGGAATACAAACA 280
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 13

AT002063
LOCUS AT002063 230 bp mRNA EST 10-AUG-1999
DEFINITION AT002063 Flower bud cDNA Brassica rapa subsp. pekinensis cDNA clone RF0337, mRNA sequence.
ACCESSION AT002063
VERSION AT002063.1 GI:5724847
KEYWORDS EST.
SOURCE Chinese cabbage.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 230)
Ryu,S.W., Lim,C.O. and Cho,M.J.
REFERENCE Brassica EST (Flower bud cDNA)
AUTHORS Unpublished (1999)
JOURNAL Contact: Cho MJ
COMMENT Department of Biochemistry
Gyeongsang National University
#900 Gajwa-dong, Chinju, Gyeongnam 660-701, Korea
Tel: 82-591-751-5957
Fax: 82-591-759-9363
Email: mjcho@nongae.gsnu.ac.kr
Submitted through BRIC(Biological Research Information Center) of
Korea
URL: <http://bric.postech.ac.kr/>.

FEATURES
source Location/Qualifiers
1..290
/organism="Brassica rapa subsp. pekinensis"
/db_xref="taxon:51351"
/clone="RF0337"
/clone_id="Flower bud cDNA"
/lab_host="MC1061"
/note="Vector: pBluescript KS(+); Site 1: EcoRI; Site 2:
XhoI; average insert size:700 bp; initial pfu:5.400 x 10
9"

BASE COUNT 85 a 70 c 60 g 75 t
ORIGIN

Query Match 40.5%; Score 102.8; DB 28; Length 290;
Best Local Similarity 62.9%; Pred. NO. 1.7e-21;
Matches 149; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

OY 17 ctaaggaatgnaatgnaatgagccaanccgaacacagtcagcttcaagctactgct 76
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 4 CTGACAAAATGATTAACCAACAAACAGCTCAAGCTTCCACCTTCCTCTCTC 63
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 77 ttccctcnaactcgcaccttccttcattcgtgagatcttcctcgaagagatcgaaga 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 64 TCTTCTCACTCACTCACTCCCTTGCTTCTCTGAGATCTTCTTGAAGCATTTGGAAGG 123
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 137 tggatggaagagcggnttggtggtctancgccatttggaagagtgtaagaaagcggtac 196
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 124 TGGATGGAAGAGCAGTGGCTTATCTGATTGGAAGAAACGAAAGCAAGCTGATC 183
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 197 ctcaagacacacagcaggaagaaatggtctggtgagatcngatgaacaaaggtcttcagac 253
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 184 CTTTAAGCACACCGCGGCAAAATGGCCCGCGCATGCCGACATATAAGTATCCAGAC 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14

AT001761
LOCUS AT001761 411 bp mRNA EST 14-JUN-1999
DEFINITION AT001761 Flower bud cDNA Brassica rapa subsp. pekinensis cDNA clone RF0156, mRNA sequence.
ACCESSION AT001761
VERSION AT001761.1 GI:5056232
KEYWORDS EST.
SOURCE Chinese cabbage.
ORGANISM Brassica rapa subsp. pekinensis
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Brassicales: Brassicaceae: Brassica 1 (bases 1 to 411)	Ryu, S. W., Lim, C. O. and Cho, M. J.	Brassica EST (Flower bud cDNA)	Unpublished (1999)	Contact: Cho, M.J.

FEATURES	Location/Qualifiers
Source	1411

BASE COUNT	121 a	104 c	82 g	104 b
ORIGIN				

Query Match	40.58;	Score 102.8;	DB 28;	Length 411;
Best Local Similarity	62.98;	Pred. No. 1.9e-21;		
Matches 149;	Conservative 0;	Mismatches 88;	Indels 0;	Gaps 0

Oy 17 cttgaagaaatgnaatgycgaanmgcaacttgaactgcgttcgaacttactgnc 76
 Db 4 CTGAGAAAAAATGAGATTATACCGCAAAACAGCTCAACCTTTCTGCGACCTC 8
 Oy 77 ttcccttcnaactctgcgcacatgggagatcttgcgttcgaacttcgaactg 36
 Db 64 TCTTCTACCTTAATGCCCTTCGCTTCGCTCTGAGATCTTCTTGAAGACATTTGAA 12
 Oy 137 tggatlggaagagccgnttgggtgcctanccgatctgaaagaagatgaagaaagcggtac 19
 Db 124 TGGATGGAAGAGCAGGTGGCTTATCTGATTGGAGAAAGAAACGAAGCAAGCTGGTAC 183
 Oy 197 cttcaagacacagcaggaabaatgtcttggtgacatcgatgaacaaagtccttcagac 253
 Db 184 CTTTAAACACACCGCCGGCAATATGCCCGGAGATCCCGACATTAAGGTATCCAGAC 240

RESULT 15			
AM624478			
LOCUS	564 bp	mRNA	EST
DEFINITION	EST3232423 tomato flower buds 3-8 mm, Cornell University		
	Lycopersicon esculentum cDNA clone, CT0B15N2.5', mRNA sequence		
ACCESSION	AM624478.1	GI:7337505	
VERSION	EST.		
KEYWORDS	EST.		
SOURCE	tomato.		

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
van der Hoeven, R.S., Bezzevredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Konning, C.M., Niemman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D.		Generation of ESTs from tomato flower tissue, 3-8 mm buds		
Unpublished (1999)		Contact: David Frisch		
		Clemson University Genomics Institute		
		100 Jordan Hall, Clemson, SC 29634, USA		

Tel: 864 656 4366
Fax: 864 656 4293
Email: dfrische@LEWSON.EDU
5 prime sequence.

```

/organism="Lycopersicon esculentum"
/cultivar="TA96"
/db_xref="taxon:4081"
/clone="CFOB15N2"
/clone_lib="tomato flower buds 3-8 mm, Cornell University"
/tissue_type="flower"
/dev_stage="3-8mm buds"
/ncbi_vector="pBluescript SK(-): Site.1: EcoRI; Site.2: XhoI; supplier: Tanksley; Flower buds and flowers were taken from greenhouse plants (4-8 wks old, TA96c). They were immediately frozen in liquid nitrogen and then size-separated while remaining frozen."
BASE COUNT      191 a      100 c      128 g      145 t
ORIGIN

```

Query Match	39.28	Score 99.6	DB 93	Length 564
Best Local Similarity	74.18	Pred. No. 2e-20		
Matches 123, Conservative	0	Mismatches 43	Indels 0	Gaps 0

[illegible]

```
Search completed: March 18, 2001, 07:37:32
Job time: 1289 sec
```

This Page Blank (empty)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic acid - nucleic acid search, using sw model

Run on: March 18, 2001, 07:22:38 ; Search time 53.84 Seconds
(Without alignments)
760.303 Million cell updates/sec

Title: US-09-199-129A-1
Perfect score: 254
Sequence: 1 ggaatcgaagctaccta.....atgaacaaagcttcagaca 254

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 280836 seqs, 80580151 residues
1 number of hits satisfying chosen parameters: 561672

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/2/lna/5A_COMB.seq:*
2: /cgn2_6/prodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/prodata/2/lna/6_COMB.seq:*
4: /cgn2_6/prodata/2/lna/PCRTS_COMB.seq:*
5: /cgn2_6/prodata/2/lna/Backfile1.seq:*

Pred. No. is the number of results predicted to have a score greater than or equal to the score of the hit. The score and is derived by analysis of the total score.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	33.6	13.2	7218	1	US-08-232-463-14
2	30.8	12.1	2518	3	US-09-433-699-3
3	29.2	11.5	3046	1	US-08-726-725-1
4	28.4	11.2	500	2	US-08-967-101-47
5	28.4	11.2	500	2	US-08-592-541-47
6	28.4	11.2	500	3	US-09-124-698-47
7	28	11.0	3303	1	US-08-081-610-3
8	28	11.0	6395	2	US-08-687-559-2
9	28	11.0	6395	2	US-09-259-741-1
10	28	11.0	6395	3	US-09-037-751-1
11	28	11.0	6425	3	US-09-259-741-3
12	28	11.0	6425	3	US-09-037-751-3
13	28	11.0	6439	3	US-09-259-741-2
14	28	11.0	6439	3	US-09-037-751-2
15	28	11.0	6446	3	US-09-259-741-5
16	28	11.0	6446	3	US-09-037-751-5
17	28	11.0	6475	3	US-09-259-741-4
18	28	11.0	6475	3	US-09-037-751-4
19	27.6	10.9	8937	2	US-08-449-933-3
20	27.6	10.9	8937	2	US-08-449-933-1
21	27.6	10.9	10706	1	US-08-411-389-1
22	27.4	10.8	43676	3	US-09-356-952-12
23	26.8	10.6	1211	3	US-08-956-182-12
24	26.8	10.6	1248	3	US-08-956-182-39
25	26.8	10.6	1365	3	US-08-956-182-27
26	26.8	10.6	1307	3	US-08-956-182-40
27	26.8	10.6	7218	1	US-08-232-463-14
28	26.8	10.6	87350	3	US-08-781-891-19

C 29	26.6	10.5	4002	1	US-08-331-488A-1	Sequence 1, Appl 1
C 30	26.4	10.4	780	1	US-08-325-553-27	Sequence 27, Appl 1
C 31	26.4	10.4	780	2	US-08-394-152A-27	Sequence 27, Appl 1
C 32	26.4	10.4	2939	2	US-08-560-398-11	Sequence 11, Appl 1
C 33	26.2	10.3	340	3	US-08-441-971-21	Sequence 21, Appl 1
C 34	26.2	10.3	340	3	US-08-441-971-22	Sequence 22, Appl 1
C 35	26.2	10.3	975	3	US-09-015-754-1	Sequence 1, Appl 1
C 36	26.2	10.3	1254	3	US-09-015-754-3	Sequence 3, Appl 1
C 37	26.2	10.3	2721	3	US-08-921-895-1	Sequence 1, Appl 1
C 38	26	10.2	1157	3	US-08-215-083-1	Sequence 1, Appl 1
C 39	26	10.2	1157	3	US-08-900-026-1	Sequence 1, Appl 1
C 40	26	10.2	6605	1	US-08-769-309A-4	Sequence 4, Appl 1
C 41	26	10.2	6605	3	US-08-994-570-4	Sequence 4, Appl 1
C 42	25.8	10.2	846	3	US-09-154-874-1	Sequence 1, Appl 1
C 43	25.8	10.2	4739	3	US-08-685-871-1	Sequence 1, Appl 1
C 44	25.6	10.1	1395	3	US-08-467-023-140	Sequence 140, Appl 1
C 45	25.6	10.1	1410	3	US-08-467-023-139	Sequence 139, Appl 1

ALIGNMENTS

RESULT 1
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29 768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-F15
US-08-232-463-14

Query Match 13.2%; Score 33.6; DB 1; Length 7218;

```

Best Local Similarity 4.5%; Pred No. 0.032;
Matches 6; Conservative 85; Mismatches 43; Indels 0; Gaps 0

OY 111 attcttcgaagagagattcgaagtgtgaaagacccnltgggtctanccgatgg 170
    |||| | : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1443 ATTGTGTCACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1384

OY 171 aaaagagtgaaaggaaaagcggtgtaccttcaagcacacgcgcggaataatggctgggat 230
    RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1324
Db 1363 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1324

OY 231 ccngatgacnaag 244
    :: :: ::::
Db 1323 RRRRRRRRRRRRRRR 1310

RESULT 2
US-09-433-699-3
Sequence 3, Application US/09433699B
Patent No. 6165786
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
FILE REFERENCE: RTS-0109
CURRENT APPLICATION NUMBER: US/09/433,699B
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 3
LENGTH: 2518
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (112)..(2235)
US-09-433-699-3

Query Match 12.1%, Score 30.8; DB 3; Length 2518;
Best Local Similarity 51.6%; Pred. No. 0.19;
Matches 65; Conservative 0; Mismatches 61; Indels 0; Gaps 0

OY 52 agtcactgcctcaagactactgncctttlccctcnaactctgcacccttcactcgtgaga 111
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1271 agaagagcgagatgctgcggaacaacttggctcaaaaattccttcaagaagtcacagg 1330

OY 112 ttcttcgaagagagatctgaagatgtgaaagacccnltgggtctanccgatgg 171
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
    1331 atgaattgaagaaagtgcttgaagatctgcggaatcagatcagattagtcgaagaagatgg 1390
OY 172 aaagga 177
    |||| |
Db 1391 aaagta 1396

RESULT 3
US-08-726-725-1
Sequence 1, Application US/08726725
Patent No. 5773290
GENERAL INFORMATION:
APPLICANT: Gould, Michael N.
TITLE OF INVENTION: MAMMARY GLAND-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles & Brady
STREET: 411 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: U.S.A.
ZIP: 53202-4497
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
```

```

COMPUTER : IBM PC compatible
OPERATING SYSTEM : PC-DOS/MS-DOS
SOFTWARE : Patent In Release #1.0 , Version #1.25
CURRENT APPLICATION DATA :
APPLICATION NUMBER : US/08/726,725
FILING DATE :
CLASSIFICATION : 435
ATTORNEY/AGENT INFORMATION :
NAME : Baker, Jean C.
REGISTRATION NUMBER : 35,433
REFERENCE/DOCKET NUMBER : 960296.93863
TELECOMMUNICATION INFORMATION :
TELEPHONE : (414) 277-5709
TELEFAX : (414) 271-3552
INFORMATION FOR SEQ ID NO : 1 :
SEQUENCE CHARACTERISTICS :
LENGTH : 3046 base pairs
TYPE : nucleic acid
STRANDEDNESS : double
TOPOLOGY : linear
MOLECULE TYPE : DNA (genomic)
US-08-726-725-1

Query Match      11.5% Score 29.2; DB 1; Length 3046;
Best Local Similarity 50.0%; Fred.No. 0.78;
Matches   67; Conservative    0; Mismatches  67; Indels    0; Gaps     0;

Qy       66 gctacttgaccttcctccatcnaacctgcagcttcatcgctgtagagtltctcgaaag 125
          | ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| 
Db        1964 gatgccittttctgtttctttttctttttttttttttttttttttttttttttggcttcg 2023

Qy       126 agattcgagaatlgaaggagaccnbtgytgtcancgcattggaataagagagtlgaaga 185
          |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| 
Db         2024 tttttcgagagctggagaccaaacccaggggatgccttttaagagagcatactaaga 2083
          || || || || || || || || || || || || || || || || || || 

Qy       186 aaagcgggtacctt 199
          || || || || || || || || || || || || || || || || || || || || || 
Db         2084 gaagctggagacctt 2097


RESULT      4
US-08-967-101-47/c
; Sequence 47, Application US/08967101
; Patent No. 5840540
GENERAL INFORMATION :
APPLICANT : ST. GEORGE-HYSLOP, PETER H
APPLICANT : ROMMENS, JOHANNA M
APPLICANT : FRASER, PAUL E
TITLE OF INVENTION : GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES : 183
CORRESPONDENCE ADDRESS :
ADDRESSEE : TESTA, HURWITZ & THIBEAULT
CITY : Boston
STREET : High Street Tower - 125 High Street
STATE : Massachusetts
COUNTRY : U.S.A.
ZIP : 02110
COMPUTER READABLE FORM :
MEDIUM TYPE : Floppy disk
COMPUTER : IBM PC compatible
OPERATING SYSTEM : PC-DOS/MS-DOS
SOFTWARE : Patent In Release #1.0 , Version #1.30
CURRENT APPLICATION DATA :
APPLICATION NUMBER : US/08/967,101
FILING DATE : 10-Nov-1997
CLASSIFICATION : 435
PRIOR APPLICATION DATA :
APPLICATION NUMBER : 08/592,541
FILING DATE :
ATTORNEY/AGENT INFORMATION :
NAME : Pitcher, Edmund R.
```


QY 230 tccnagatgacnaaggtcttcagac 253
Db 117 TCCTCATTAACACTGACTAGGCC 94

RESULT 7
US-08-081-610-3
Sequence 3, Application US/08081610
Patent No. 5445941
GENERAL INFORMATION:
APPLICANT: Yang, Na N
TITLE OF INVENTION: Materials and Methods for Screening
TITLE OF INVENTION: Anti-Osteoporosis or Serum Lipid Lowering Agents
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 S. Wacker Dr.
CITY: Chicago
STATE: IL
COUNTRY: U.S.A
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/081,610
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Heaphy, Barbara A
REGISTRATION NUMBER: 34,619
REFERENCE/DOCKET NUMBER: 93,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: mRNA
LOCATION: 2170..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2214..3303
FEATURE:
NAME/KEY: mRNA
LOCATION: 2219..3303
FEATURE:
NAME/KEY: misc_RNA
LOCATION: 3301..3303
OTHER INFORMATION: /note= "CDS Start, codon start = 1,
OTHER INFORMATION: translation M"
FEATURE:
NAME/KEY: TATA_signal
LOCATION: 2170..2176
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1896..2306
OTHER INFORMATION: /note= "pb-301 -301 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1976..2306
OTHER INFORMATION: /note= "pb-221 -221 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2106..2306
OTHER INFORMATION: /note= "pb-91 -91 to +110"

FEATURE:
NAME/KEY: misc_feature
LOCATION: 2137..2306
OTHER INFORMATION: /note= "pb-60 -60 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2150..2306
OTHER INFORMATION: /note= "pb-47 -47 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2159..2306
OTHER INFORMATION: /note= "pb-38 -38 to +110"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2159..2271
OTHER INFORMATION: /note= "TGFB-3 position -38 to
OTHER INFORMATION: +75"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2159..2231
OTHER INFORMATION: /note= "TGFB-3 position -38 to
OTHER INFORMATION: +35"
US-08-081-610-3

Query Match 11.0%; Score 28; DB 1; Length 3303;
Best Local Similarity 59.0%; Pred. No. 2.2;
Matches 46; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 170 gaaagaggtgaaggaaggggtaccttcagacacagaggaatgctgggga 229
Db 1229 GAAGAGGAGCGAAGACGACGACCTTCCCTCACCCTATCTGGGAATGCTCGGCC 1288

QY 230 tccnagatgacnaaggtct 247
Db 1289 AACTGCTGACTTCGGCCT 1306

RESULT 8
US-08-687-559-2
Sequence 2, Application US/08687559
Patent No. 5955647
GENERAL INFORMATION:
APPLICANT: Fitcher, John H.
APPLICANT: Beachy, Roger N.
TITLE OF INVENTION: METHOD FOR USING TOBACCO MOSAIC VIRUS TO
TITLE OF INVENTION: OVERPRODUCE PEPTIDES AND PROTEINS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,559
FILING DATE: No. 5955647ember 18, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01467
FILING DATE: 03-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Learn, June M.
REGISTRATION NUMBER: 31,238
REFERENCE/DOCKET NUMBER: 07302/011001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070

MOLECULE TYPE: Genomic RNA

Oy 132 gaagatcgtatcgaaagaccgntctgtctctnccgatcttgaaaaggagtgaagaataaacgcg 191
| ||||| | | | | | | | | : | | |
Db 3059 GGAGAGGCGCCGGACGCCGUGAUCANUCCGANCUCCAAAACCUCUUGCANGGCAGAU 3118

OY 192 ggtaccttcacagcacagcgaggaatgctctg 225
Db 3119 CCUGACUUUUAACCAUCCGGAUUAAGAAGCUCUG 3152

RESULT 11

US-09-259-741-3
Sequence 3, Application US/09259741
Patent No. 6033895

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN
APPLICANT: HOLTZ, R. BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: SOURCES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259,741
FILING DATE: February 25, 1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,751
FILING DATE: March 10, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.US01

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400

TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 6425 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: unknown

MOLECULE TYPE: Genomic RNA
US-09-259-741-3

Query Match 11.0%; Score 28; DB 3; Length 6425;
Best Local Similarity 46.8%; Pred. No. 3.1;
Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;

OY 132 gaagatgagtggaagagcggtgtgctanccgattgaaagagtggaagaaacgcg 191
Db 3059 GGAGAGUGGUGCGGAGCGCGCGGAGUCCAGCAUCCGAAACCCUUGCAUGGCAAGAU 3118

OY 192 ggtaccttcacagcacagcgaggaatgctctg 225
Db 3119 CCUGACUUUUAACCAUCCGGAUUAAGAAGCUCUG 3152

RESULT 12

US-09-037-751-3
Sequence 3, Application US/09037751
Patent No. 6037456

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN
APPLICANT: HOLTZ, R. BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES
TITLE OF INVENTION: FROM PLANT SOURCES
NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,751
FILING DATE: 10-MAR-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P
REGISTRATION NUMBER: 25,277

REFERENCE/DOCKET NUMBER: 00801.0140.999

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400

TELEX:

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 6425 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: unknown

MOLECULE TYPE: Genomic RNA
US-09-037-751-3

Query Match 11.0%; Score 28; DB 3; Length 6425;
Best Local Similarity 46.8%; Pred. No. 3.1;
Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;

OY 132 gaagatgagtggaagagcggtgtgctanccgattgaaagagtggaagaaacgcg 191
Db 3059 GGAGAGUGGUGCGGAGCGCGCGGAGUCCAGCAUCCGAAACCCUUGCAUGGCAAGAU 3118

OY 192 ggtaccttcacagcacagcgaggaatgctctg 225
Db 3119 CCUGACUUUUAACCAUCCGGAUUAAGAAGCUCUG 3152

RESULT 13

US-09-259-741-2
Sequence 2, Application US/09259741
Patent No. 6033895

GENERAL INFORMATION:

APPLICANT: GARGER, STEPHEN
APPLICANT: HOLTZ, R. BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURPEN, THOMAS

TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: SOURCES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:


```

Query Match Similarity 11.0%; Score 28; DB 3; Length 6439;
Best Local Similarity 46.8%; Pred No. 3.1;
Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;

QY 132 gaagatgagtcgaagagaccgntgggtgctcancgattggaagaagagtcgaagaaagcg 191
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3059 GGAGAGUGCGCGCGGAGCGCGCGCGUGCAUCCAUAUCCGAUCCGAUCCUCAAACCCUUGCAUCCGAU 3118

OY 192 ggtacctcaagcacacagcgaggaatgctg 225
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3119 CCUGACUUUUVACCACCAUCCGGAUAGAGAGCCUCUG 3152

RESULT 15
US-09-259-741-5
: Sequence 5, Application US/09259741
: Patent No. 6038695

GENERAL INFORMATION:
APPLICANT: GARGER, STEPHEN
APPLICANT: HOLTZ, R. BARRY
APPLICANT: MCCULLOCH, MICHAEL
APPLICANT: TURPEN, THOMAS
TITLE OF INVENTION: A PROCESS FOR ISOLATING AND
PURIFYING VIRUSES SOLUBLE PROTEINS AND PEPTIDES FROM PLANT
TITLE OF INVENTION: SOURCES
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/259, 741
FILING DATE: February 25, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037, 751
FILING DATE: March 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P

```

```

: REGISTRATION NUMBER: 25,277
: REFERENCE/DOCKET NUMBER: 00801.0140.US01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-463-8100
: TELEFAX: 650-463-8400
: TELEX:
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6446 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: unknown
: MOLECULE TYPE: Genomic RNA
: US-09-259-741-5

```

```

Query Match      11.0%; Score 28; DB 3; Length 6446;
Best Local Similarity 46.8%; Pred. No. 3.1;
Matches 44; Conservative 8; Mismatches 42; Indels 0; Gaps 0;

132 gaagatgagatgaaagagcagntgggtgctanccgattgaaagagatgaaagaaagcg 191
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3059 GGAGAUUGGUGCGGAGCGCGCGGUGAUCAUCCGAUCUCAAACCCUUGGCAAGCAU 3118
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 192 ggtatctcaagcacacagcaggaatggtctg 225
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 3119 CCUGACUUUUAUCCCAUCCGAUAAAGAACUCUCG 3152
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: March 18, 2001, 08:26:06
 Job time: 3808 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2001, 07:17:18 ; Search time 954.67 Seconds
(without alignments)
1361.631 Million cell updates/sec

Title: US-09-199-129A-1

Perfect score: 254
Sequence: 1 ggaatctgaagctacctta.....atgacnaagctctcagaca 254

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1118133 seqs, 2558875100 residues

number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_bal: *
2: gb_bal: *
3: gb_bal: *
4: gb_bal: *
5: gb_bal: *
6: gb_bal: *
7: gb_bal: *
8: gb_bal: *
9: gb_bal: *
10: gb_bal: *
11: gb_bal: *
12: gb_bal: *
13: gb_bal: *
14: gb_bal: *
15: gb_bal: *
16: gb_bal: *
17: gb_bal: *
18: gb_bal: *
19: gb_bal: *
20: gb_bal: *
21: gb_bal: *
22: gb_bal: *
23: gb_bal: *
24: gb_bal: *
25: gb_bal: *
26: gb_bal: *
27: gb_bal: *
28: gb_bal: *
29: gb_bal: *
30: gb_bal: *
31: gb_bal: *
32: gb_bal: *
33: gb_bal: *
34: gb_bal: *
35: gb_bal: *
36: gb_bal: *
37: gb_bal: *
38: gb_bal: *
39: gb_bal: *
40: gb_bal: *
41: gb_bal: *
42: gb_bal: *
43: gb_bal: *

44: em_hcg8: *
45: em_hcg9: *
46: em_hcg10: *
47: em_hcg11: *
48: em_hcg12: *
49: em_hcg13: *
50: em_hcg14: *
51: em_hcg15: *
52: em_hcg16: *
53: em_hcg17: *
54: em_hcg18: *
55: em_hcg19: *
56: em_hcg20: *
57: em_hcg21: *
58: em_hcg22: *
59: em_hcg23: *
60: em_hcg24: *
61: em_hcg25: *
62: em_hcg26: *
63: em_hcg27: *
64: em_hcg28: *
65: em_hcg29: *
66: em_hcg30: *
67: em_hcg31: *
68: em_hcg32: *
69: em_hcg33: *
70: em_hcg34: *
71: em_hcg35: *
72: em_hcg36: *
73: em_hcg37: *
74: em_hcg38: *
75: em_hcg39: *
76: em_hcg40: *
77: em_hcg41: *
78: em_hcg42: *
79: em_hcg43: *
80: em_hcg44: *
81: em_hcg45: *
82: em_hcg46: *
83: em_hcg47: *
84: em_hcg48: *
85: em_hcg49: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	95.6	37.6	1424	7	ATU66345
2	77	30.3	1564	7	BVNRNAC
3	76.4	30.1	1545	6	AF190454
4	76.2	30.0	1463	7	ATU66343
5	75.6	29.8	1547	6	AF052040
6	75.6	29.8	1593	7	AF283816
7	74.4	29.3	1558	33	NPCALIMNR
8	74	29.1	1450	7	BLYCRH2A
9	74	29.1	1472	7	BLYCRH1A
10	74	29.1	1558	6	AB021259
11	72.6	28.6	1514	33	RCU74630
12	72.6	28.6	1543	7	CAPCRIC
13	72	28.3	89479	6	AC006932
14	71.6	28.2	1614	33	ZMCRALPREC
15	70	27.6	1342	33	ZMCRALPREC
16	70	27.6	1413	7	ATU27698
17	69.4	27.3	1524	6	AF134733
18	66.8	26.3	1170	33	NTRNATCAL
19	65.6	25.8	262	78	RICL819A
20	65.2	25.7	1600	6	AF019376
21	56.2	22.1	1363	32	DDU36937

C 22	54.2	21.3	98616	67	AC058785	Arabidops
C 23	54.2	21.3	112448	69	AC069159	Arabidops
C 24	53.4	21.0	2038	7	AT066344	Arabidops
C 25	53.4	21.0	59261	33	T12M4	Arabidops
C 26	51.4	20.2	49261	33	RC0474631	Arabidops
C 27	43.6	17.2	742	6	AB018243	Rattus norvegicus
C 28	43.6	17.2	2336	7	CRAJ765	Arabidops
C 29	37	14.6	98616	67	AC058785	Arabidops
C 30	35	13.8	195154	62	AC022246	Arabidops
C 31	35	13.8	276042	57	AC012183	Arabidops
C 32	34.6	13.6	22842	31	CEP75	Arabidops
C 33	34.6	13.6	159639	55	AC008747	Arabidops
C 34	34.6	13.6	160026	61	AC021437	Arabidops
C 35	34.4	13.5	136519	66	AC034229	Homo sapi
C 36	34.2	13.5	95683	57	AC011796	Homo sapi
C 37	34.2	13.5	205839	57	AC013350	Mus muscu
C 38	34	13.4	109614	68	AC064850	Homo sapi
C 39	34	13.4	183628	57	AC012245	Homo sapi
C 40	33.8	13.3	43345	58	AC014886	Drosophila
C 41	33.8	13.3	80074	54	AC008389	Homo sapi
C 42	33.8	13.3	84970	54	AC008388	Homo sapi
C 43	33.8	13.3	86581	52	AC016426	Homo sapi
C 44	33.8	13.3	101076	59	HS37M17	Homo sapi
C 45	33.8	13.3	106926	54	AC007651	Drosophila

ALIGNMENTS

ORIGIN	Query Match	37.6%;	Score 95.6;	DB 7;	Length 1424;
	Best Local Similarity	75.3%;	Pred. No. 8.3e-20;		
	Matches 116;	Conservative	0;	Mismatches 38;	Indels 0;
				Gaps	
QY	100	cattcgctgagatcttccttcgaaagagatcttcgaagatgtagtaagaaagcgcnttggtgc	159		
Db	99	CTTCTCTCCGAGATCTTCTTAGAGGAGCATTTTCGAGGTGATGCAAAAGTAGTGGCTC	158		
QY	160	tanccgaattggaagaagagtgaaagaaagcgggtaccttcacagcacacagcaggaatat	219		
Db	159	TGCTGTATTGGAAAAAGAAAGCAAGGCNAACCTTGAACCTTTAAGCACACCTGCCGGTAAT	218		
QY	220	ggtctggggtccngatgacmaaggtcttcaagc	253		
Db	219	GGCCCGGCGATCCTGACATAAAGGTATTCAGAC	252		
RESULT	2				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calreticulin.				
LOCUS					
BYRNAC					
BYRNAC	1564 bp	mrna			
LOCUS					
DEFINITION	Beta vulgaris mRNA for calret				

RESULT	1
LOCUS	ATU66345
DEFINITION	Arabidopsis thaliana calreticulin (Crt3) mRNA, complete cds.
ACCESSION	U66345
VERSION	U66345.1
KEYWORDS	GI:2052382
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE	1 (bases 1 to 1424) Nelson,D.E., Glaunsinger,B. and Bohnerl,H.J. Abundant accumulation of the calcium-binding molecular chaperone calreticulin in specific floral tissues of Arabidopsis thaliana Plant Physiol. 114 (1), 29-37 (1997)
AUTHORS	2 (bases 1 to 1424) Nelson,D.E., Glaunsinger,B. and Bohnerl,H.J. Direct Submission Submitted (07-AUG-1996) Biochemistry, University of Arizona, Bioscience West 513, Tucson, AZ 85721, USA
JOURNAL	Location/Qualifiers
MEDLINE	1. 1424
WORDS	/organism="Arabidopsis thaliana"
REFERENCE	/db_xref="taxon:3702"
LOCUS	23. 1297
gene	/gene="Crt3"
CDS	23. 1297
	/gene="Crt3"
	/codon_start=1
	/product="calreticulin"
	/protein_id="AAC49697.1"
	/db_xref="GI:2052383"
	/translation="MGLPQNKLSFECFFVLVTLPAPLAFSEIFLEEHREGNKSRLV VLSDDKRNKRGACGFTKHTPAKWPDPDNKGIQYVNDKAKVAISAKIPEFSKNKNTLVV QYSAKIEQDIECGGAYIKLSGYVNGQKFGSDPYSLMKGEGISGDTQTKLHVIVSYG GQNPVPIKDDQCECTDKLNHFYTFILRPDASVYSLMKGREGSGMTDMDLTPRKIK VNAAKRGKEDMDREYIDDPNDVKMEGDSIPRELPDRAKPEMDDEENGILMPKPKI PNVAKRGKAKAKRIKNNPYGKMKMKNPMDNDPEDDDLVYKSTYAGTIVWPKKAG SIFDNLITCDDPARASIVDPYPAQHESKEKELFAEAEKKEKKADEBARAKEEGE RKREDRIRYCDRRKRIKRPMDIMDYHDEL"
BASE COUNT	449 a 259 c 350 g 366 t

	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Caryophyllidae; Caryophyllales; Chenopodiaceae; Beta.
REFERENCE	1 (bases 1 to 1564)
AUTHORS	Viereck, R.
TITLE	Direct Submission
JOURNAL	Submitted (15-OCT-1997) Viereck R., Universitaet Heidelberg, Botanisches Institut, Im Neuenheimer Feld 360, 69120 Heidelberg, GERMANY
REFERENCE	2 (bases 1 to 1564)
AUTHORS	Viereck, R.
TITLE	Nucleotide sequence from sugar beet calreticulin
JOURNAL	Unpublished
FEATURES	Location/Qualifiers
SOURCE	1..1564 /organism="Beta vulgaris" /strain="diploide Inzuchtlinie KWS; Partle: VV-D/2R5" /db_xref="taxon:3555" /clone_id="Lambda ZAP Express" /rfeature="leaf" 20..1270 /codon_start=1 /product="calreticulin" /protein_id="CAA05161.1" /db_xref="GI:3288108" /db_xref="SPTRMBL:081919" /translation="MENGRKNSPFLSLLLLSFAISAKYFEERFEDGMEKRMRVKS EMWKEDEMAEWMVTSGKNMGDANDKDICIQSEDFRAISAEPPEFSNKONTLVFOES HLIEKKIDPCETDQLHWYTEILRLRDAYTEFLIDNEOKGTGLYDMDLPAKRIKDP AKRPEDMDKEFIIPDDPKRKPEGYDIIPAETTPDEAKRPEDMDEEGEWAVPIPNP EYGEPMFKARKIKNPNTYKGSKMKAPIMDNPEFRDDELIVPKIRYGVGLMQVKSGTLE DNVLVDDEPYAQOLAEFTYGKCKORDAKKAPEELKKRREEETRYODPVESADEDDE EAUDSDDDDDKSDDKDDDDHDEL"
CDS	
BASE COUNT	493 a 307 c 375 g 389 t
ORIGIN	
Query Match	30.3%; Score 77; DB 7; Length 1564;
Best Local Similarity	57.9%; Pred. No. 7.3e-14;
Matches 128; Conservative	0; Mismatches 93; Indels 0; Gaps 0;
3 atggccaanmcgaacactagatcgcgtcaagaactgcttcttcctnaactctg 92	

[illegible]

OY	228	gattcngatgacnaaggtcttcaggc	253
Dd	273	GATGCCGAGGACAAAGATTTCAAAC	298
RESULT	4		
LOCUS	ATU66343	1463 bp	mRNA PLN 28-Apr-1997
DEFINITION	Aralbidopsis thaliana calreticulin (Crli) mRNA, complete cds.		
ACCESSION	U66343		
VERSION	U66343.1	GI:2052378	
KEYWORDS			
SOURCE	thale cress.		
ORGANISM	Aralidopsis thaliana		
	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;		
	Brassicales; Brassicaceae; Arabidopsids.		
REFERENCE	1 (bases 1 to 1463)		
AUTHORS	Nelson,D.E., Glaunsinger,B. and Bohnert,H.J.		
TITLE	Abundant accumulation of the calcium-binding molecular chaperone calreticulin in specific floral tissues of Arabidopsis thaliana		
JOURNAL	Plant Physiol. 114 (1), 29-37 (1997)		
MEDLINE	97303616		
REFERENCE	2 (bases 1 to 1463)		
AUTHORS	Nelson,D.E., Glaunsinger,B. and Bohnert,H.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (07-AUG-1996) Biochemistry, University of Arizona,		
FEATURES	Biosciences West 513, Tucson, AZ 85721, USA		
SOURCE	Location/Qualifiers		
	1..1463		
	/organism="Arabidopsis thaliana"		
	/db_xref="taxon:3702"		
gene	4..1281		
CDS	/gene="Crli"		
	4..1281		
	/gene="Crli"		
	/codon_start=1		
	/product="calreticulin"		
	/protein_id="AAC49695.1"		
	/db_xref="GI:2052379"		
	/translation="MAKLNPKFISLLIFALVIVISAETIEPERPEDGMEXRMVKSDMKKDNMTAGEMKRTTACNMSGDANDKRITQISEDRFAIASEPPEFSNKDKTLVFQSYVRKEQLDGGGTAKLISDDVDQRFEGDPYSIMFGPDICGVSTSKVAHILTYNGTNHLILKEVECFEIDQLTHVTTFVLRPDATYSLINDVEQTGLSIDMDLTPAKIKPSARKEPEDMDKKXIYPEDPTCPAGYDDIPKEIPDTDAKPEDMDEEDGEWTAPIIPMEYNVGEPMFKIKNPAYIGXKMKAAPIDNPERFDDELVPRLKYGVELMOVSGSLFDNVLVSDPEPAKLAEETGKHIDAKKAAPDEAKEERREESDNAESADEEAADDONNEGDSNSNSESETEAREAFETKEAETDAHELF."		
BASE COUNT	456 a 279 c 368 g 360 t		
ORIGIN			
	Query Match	30.0%:	Score 76.2; DB 7; Length 1463;
	Best Local Similarity	68.5%:	Pred. NO.1.3e+13;
	Matches 102; Conservative	0;	Mismatches 47; Indels 0; Gaps 0;
Oy	105	gctgaagtcttcttcgaagaagatcgaaatgataggaaagccgnltgggtcanc	164
Dd	67	GCTGAAGTTATCTTGAGAGCAAAATTCCAGAATGATGGAGACAAGATGGTTAAATCT	126
Oy	165	gattgaaaaggagtgaaagaaaagcgggtaccctcaagcacacacagcagaanaatgctct	224
Dd	127	GACTGAGAAAAGATAAATTAATCTCCTCGGGGAATGGAACACACAGCTGAAATTTGGTCT	186
Oy	225	ggggagtcnagatgacnaaggtcttcaggc	253
Dd	187	GGTGATGCTAACGATAAAGGTATCCAAC	215
RESULT	5		
LOCUS	AF052040	1547 bp	mRNA PLN 04-MAR-1999
DEFINITION	Berberis stolonifera calreticulin mRNA, complete cds.		

ACCESSION AF052040 GI:4335863
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Berberis stolonifera.
 Berberis stolonifera
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 Magnoliophyta; eudicotyledons, Ranunculales; Berberidaceae;
 Berberis
 REFERENCE
 1 (bases 1 to 1547)
 Chou,W.-M. and Kutchan,T.M.
 Calreticulin from Berberis stolonifera
 Unpublished
 2 (bases 1 to 1547)
 Chou,W.-M. and Kutchan,T.M.
 Direct Submission
 Submitted (03-Mar-1998) Laboratorium fuer Molekulare Biologie,
 Universitaet Muenchen,裴尔strasse 29, Muenchen 80333, Germany
 Location/Qualifiers
 1..1547
 /organism="Berberis stolonifera"
 /db_xref="taxon:33814"
 /note="Cell suspension culture"
 21..1271
 /function="possible molecular chaperon"
 /note="calcium binding protein of the endoplasmic
 reticulum"
 /codon_start=1
 /product="calreticulin"
 /protein_id="AADI7490.1"
 /db_xref="GI:4335864"
 /translation="MAIAERSRHIALRVDRVSAEYFFEREEDGHSWVVSQDKK
 RDEMMAGEMNFTSGKWNGDANDKCIQTSEDYRFAISAPFEFSKGTIVFQSVKK
 EQKLDCGGTYTKLLSDVDOKRFEGSDIPYSIFEPDILCGYSTKVHALLTGEFNHL
 KKDLPCESTDLTTHYYTEILRPDAASYSLIDNVEKOSGVYDMOILLPKQIKDEPAKK
 PEDVEDEKYIPDPEDKKPEGYDDIPEKETIDEAKKPEDMDDEDGEEMTAPTIPNDYD
 GEMPKRIKNENFKGWKAAPMIQNDPDKDDPIVVPKIKVVGIELMOVKSCTMEDNNY
 LIODPPYARKLIAETPMGKNDAAKKAFADEAEKKKEBEAKADPTESDDEKPDERGES
 DGECDSDSKIDNEDEDDVHDEL"
 BASE COUNT 487 A 277 C 391 G 392 T
 ORIGIN
 Query Match 29.8%; Score 75.6; DB 6; Length 1547;
 Best Local Similarity 62.0%; Pred. No. 2e-13;
 Matches 114; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
 QY 70 ctgagcttcttcctnaactgcacgtcacttcattcgatcgagagtcttcgaaagagat 129
 || ||| || | || | || | ||| ||| ||| ||| ||| ||| ||| |||
 F 49 CTCATCTTGCGTCCTCCGTTGCCGATCGCTGTTTCGCTGAAGACTCTTTCGAAGAAGCAT 108
 [REDACTED]
 QY 130 tcgaagatlgatlggaagaagcccnltgglygtctancaccgatctggaagaagatgaagaagaag 189
 || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 109 TTGAAGATGATGGAGAGCAATAATGGATTAAATCATTGATGGAAGGGATGTGAACATGG 168
 QY 190 cgggtaccttaagcacagcagcaagaanaatgylctgggataccngatgacmaaggcttc 249
 || | || | || | || | || | || | || | || | || | || | || |
 QY 169 CCGGAGAGTGAAGACTTCACTCCGGAATAATGGAATGAGATGCTAATGAAGAAGTATCC 228
 Db 250 agac 253
 || ||
 Db 229 AAAC 232
 RESULT 6
 AF283816
 LOCUS AF283816 1593 bp mRNA PLN 21-AUG-2000
 DEFINITION Pinus taeda calreticulin mRNA, complete cds.
 ACCESSION AF283816
 VERSION AF283816.1 GI:9858813
 KEYWORDS
 SOURCE loblolly pine.
 Pinus taeda
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

REFERENCE	1	Coniferopsida: Coniferales; Pinaceae; Pinus.
AUTHORS	1 (bases 1 to 1593)	Shealy, M. J. and Frankis, R. C. Jr.
TITLE	Complete nucleotide sequence of a cDNA encoding calreticulin from Pinus taeda	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 1593)	Shealy, M. J. and Frankis, R. C. Jr.
AUTHORS	Direct Submission	
TITLE	Submitted (30-JUN-2000) Department of Biology, College of Charleston, 66 George St., Charleston, SC 29424, USA	
JOURNAL	Location/Qualifiers	
FEATURES	1. 1593	
source	/organism="Pinus taeda"	
	/db_xref="taxon:3352"	
	/tissue_type="pollen"	
	24. 1307	
	/note="calcium-binding protein"	
	/codon_start=1	
	/product="calreticulin"	
	/protein_id="AA01147.1"	
	/db_xref="GI:9858814"	
	/translation="MAGRRLSYAVFLLEVTLYSAEYFEEREDSDMESRMVOSDMKDESLAGDMVHTSGKMGNDPNDKGIQHTDVRFPALISAAYEFSKDKTLVLOEVSVKIKDLCGGGVYKLLSGEIDOKNFGSEGPYSIMFGPDICGSKTKYVHTLISYKGRKPIIKDVCEDQLHVTYFTILRPATYSILDNTDKOSGLIKKMDLLPRTIKDPAKKKEDWDKETITPDEPKKPEGVDIDPEIKETDPDPTKPEMDNDEDEGWAPTLANPEYKPKWKRKILKNPYNKGRWKAPMIDNDFKDDPELVFPNLKYGIELMVKSGTLFDNIILSDPEYAKFLAEYTMANKHDEAKAEAFDEAEKKKEEEKESDEEDTDERKEEKSDIDAEDELDEHKEADKKHEHLEDEKKEHDEL"	
BASE COUNT	532 a	267 c 382 g 412 t
ORIGIN		
Query Match	29.8%; Score 75.6; DB 7; Length 1593;	
Best Local Similarity	68.0%; Pred. No. 2.1e-13;	
Matches 102; Conservative	0; Mismatches 48; Indels 0; Gaps 0.	
QY	105 gctgagattcttcctgaaagagatcgaagaatgtagaagagccnltggtctganc	164
Db	87 GCCGAAGCTCTTTTTCGAGAGAGCGCTTCGATGACCTGGGAAAGTCGTGGTGCATCT	146
QY	165 gattggaagagagtggaaggaagacgggttacctccaagcaacgcggaagaaatgctct	224
Db	147 GATTGGAAGAAAGATGAAGACTTGCTGAGATTGCGTGACACACATCAGGAAATGGAAC	206
QY	225 gaggatccnagatcnaaggtcttcagaca	254
Db	207 GGGATCCCAATGACACAGCGCATCCAACA	236
RESULT	7	
NPICALIMNR	1558 bp	mRNA
LOCUS	NPICALIMNR	PLN
DEFINITION	N.plumbaginifolia mRNA for calreticulin.	27-JUN-1996
VERSION	271395	
KEYWORDS	271395.1	GI:1419087
SOURCE	CABI gene; calreticulin.	
ORGANISM	Nicotiana plumbaginifolia	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Asteridae; Solanales; Solanales; Solanales; Solanales; Nicotiana.	
REFERENCE	1 (bases 1 to 1558)	
AUTHORS	Borisjuk, N., Borisjuk, L., Adler, K., Sitalo, L., Twes, A. and Martenfel, R.	
TITLE	Differential expression of calreticulin during somatic and zygotic embryogenesis of Nicotiana plumbaginifolia	
JOURNAL	Unpublished	
REMARK	(sites)	
REFERENCE	2 (bases 1 to 1558)	
AUTHORS	Borisjuk, N.	
TITLE	Direct Submission	


```

/gene="CRH1"
/codon_start=1
/function="calcium binding protein"
/product="calreticulin"
/protein_id="AA32948.1"
/db_xref="GI:439586"
/translation="LLRRLLALLASVAANAADVFQDEKFEDEGSFNVKSEMKKDEEN
MAGWNHTSGKRWGHDAEDKGIQTSSEDRFAISAEYEPFSKDKTLVQLQFVKEDEOKL
DCGGGVYLLGLDQDKFGSGDPYRGYIMFGSDICGYSTKRVHTLLTNGKNNLLKIKQ
PCEDDLSHYTLTLIRBDATYSLIDNEEKOTGSIYHMWLLPKEKILDPKAPKKEDEPM
DKRYILPDPEDEVKREGYDDIPKEVTPDDAKKPEWMDDEDESGMTAPITIPNEYKGPKN
OKRTKKNPYQGMKWAPMIANDPFQDDYIYAFDSLKYLGLWQVKSGLTEFDNLLITVD
DAALATFAETWAKRHKDAEKAAPDEAEKKEEDDASKAGEDDDDLDEDAEDDDKDD
KAGSDAEDDDSDDEKDEHL"

```

Query Match	29.1%	Score 74	DB 73	Length 1472
Best Local Similarity	67.3%	Pred. No. 6.6e-13		
Matches 101	Conservative 0	Mismatches 49	Indels 0	Gaps 0

QY	104	cgcttgaattctcttcgaaagagatctcgaatgtaagaaacgntgggtctanc	163
Db	53	CGCGACGCTTCTTCCACGAGAAAGTTGGAAGATGCGTGGGAACCCGGTCAAGTC	112
QY	164	cgattgaaagagatgaaagaaacgggtacccttcaagcacacagcaggaanaatgctc	223
Db	113	TGAGTGGAAAGAGGACGCGAACAATGGCGTGTGAATGGAACACACATCTGGAAATATGCA	172
QY	224	tgggatcngatgacnaagatcttcagac	253
Db	173	TGGAGATCTCTGAGCACAAGGATATCCAAAC	202

```

RESULT 10
AB021259
LOCUS AB021259 1558 bp mRNA PLN 28-MAR-2000
DEFINITION Oryza sativa mRNA for calcium-binding protein, complete cds.
ACCESSION AB021259
VERSION AB021259.1 GI:6682832
KEYWORDS calcium-binding protein.
SOURCE Oryza sativa cDNA to mRNA.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
1 (sites)
Li,Z. and Komatsu,S.
Molecular cloning and characterization of calreticulin, a
calcium-binding protein involved in the regeneration of rice
cultured suspension cells
Eur. J. Biochem. 267 (3), 737-745 (2000)
2011/682
2 (bases 1 to 1558)
Komatsu,S. and Li,Z.
Direct Submission
Submitted (15-DEC-1998) to the DDBJ/EMBL/genbank databases.
Settsuko
Komatsu, National Institute Agrobiological Resources, Department of
Molecular Biology, Kannondai 2-1-2, Tsukuba 305-8602, Japan
(E-mail:skomatsu@agr.affrc.go.jp, Tel:81-298-38-7490,
Fax:81-298-38-7032)
1.1558
Location/Qualifiers
/organism="Oryza sativa"
/db_xref="taxon:4530"
31.1305
FEATURES
SOURCE
CDS

```

```

/codon_start=1
/product="calcium-binding protein"
/protein_id="BAAB8900.1"
/db_xref="GI:6682833"
/translation="MAIRARSSSYAAVAALALALAAVAAGVVFQOEKFEDEMER
WVSEKDEENMAGCEWNTHTSGKMGDDDEDGIQISEYRYALSAEYPERFSNKRTLY
LQSVKHEQKLDCEGGGYVKLLIGGVDDKRCGGDPTIGSTAKRVHIFPK

```

BASE COUNT 453 a 330 c 437 g 337 t 1 others
ORIGIN
NDKNNHLIKRKDVPCETTDOLSHNYTLIHPADTAYSLILINVEKSSQSYIEHMDILPPTAOI
KDPEKAPKPEBDDKDEYIPDEDDKKEGIDYDIPKTIIPDPAKPGAGDEEDGEGTAPPT
IRNEYKGPWKOKKIKRNPYOGKKPMPIMATPDODDPIYAFPSISIGELTMOVSS
GTLFDNLITLDALALATPAEETKATKKHAKDEKAFDAEKKKKEEENAKKAGEDDDDL
DEBAEDDKADEKADSDAEDGKSDSKNHDL"

Query Match	29.1%	Score 74	DB: 6	Length 1558
Best Local Similarity	67.3%	Pred. No. 6	6e-13	
Matches 101	Conservative 0	Mismatches 49	Indels 0	Gaps 0
QY 104	cgtctgaagatttctctcgaaagagagattcgaagatgtagtgaagagccgnttggtgtctanc	163		
Db .114	CGCGGAGGCTTTCTCCACGAGGAAGTTCCAGAGATGGATGGGAAATCGGTGGTCAAATC	173		
QY 164	cgatttggaagagagatgtaaggaagaaagcggtgaccttcgaagcacacagcaggaataatgttc	223		
Db 174	AGAAATGGAAAGAGGATGGGAACATGGCTGGTGTAATGGAACACACATCTGGGAATGTGAA	233		
QY 224	tggagatccgatgacnaaggtcttcagac	253		
Db 234	TGGAGATCTCTGAGGACCAAGGTATCCAAAC	263		

RESULT	11				
LOCUS	RCU74630				
DEFINITION	RCU74630	1514 bp	mRNA	PLN	29-SEP-1997
ACCESSION	U74630				
VERSION	U74630.1				
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
MEDLINE					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
FEATURES					
source					

```

/organism="Ricinus Communis"
/db_xref="taxon:3988"
7. .1254
/codon_start=1
/product="calreticulin"
/protein_id="AAB71419.1"
/db_xref="GI:1656197"
/translation="MANPKSLTFLSLIAASAEVPEEREEDGEMENRWKSDMKK
ENIAEGWNTVSGKMGNDPNKGIQTSDEYVYAIASAEFPEPSNEDKGLVQFSYKHKD
KIDCGGYSMKLLSSSTQKKFEGDTPVSIAMGPDICSTIRKHAIIINYDNTNLIRK
EVEEDTQLTHVTVLTVPATYSILIDNVEKQTSLYTDWDLTPKIKDPEAKKPEE
DMEDEKEYIPDPEDKKPGYDDIPKEIIPDPAKKREDWDDEDEMTAPTIANPEYKSP
MKRPIILNPYKGMKMAPMDINPDFKDDPELYVVPNLYKYGIELMQYKSGSLFQNVLI
CNDEPVAKOLAEETGKKNKADEKNAKFAPEAKKKKEESKDDPNADSDADEDDDDADTIE
GDDDEKSKNAADSAEDVDHDEL"

```

Query Match	28.6%	Score 72.6;	DB 33;	Length 1514;
Best Local Similarity	65.8%	Pred. No. 1.9e-12;		
Matches 102; Conservative	0;	Mismatches 53;	Indels 0;	Gaps 0;

Oy	100	cattcgctgagaatcttcttcgcgaagagatctcgaagatggagtggaagacccntggatgc	159
Db	59	CTTTCGCAAGACTTTCTTCGAGACGGCTTTCCGAAGATGCATGGCAAAATAGCTGGTTA	118
Oy	160	tanccgatctgaaaaggagtgaaggaaaaagcggtaaccttcagacacacagcaggaaaat	219
Db	119	AATCGATTGGANAGAAAGATGAGATPACAGCTGGTGATGGAATTAATACCCTGGAAAGT	178
Oy	220	ggctcggggtatcngatgacmaaggcttcagaca	254
Db	179	GGAATGGAGACCTTAATGCAAGAAGTATTCAACA	213

RESULT 12			
CARCTR	LOCUS	CAPCRMC	1543 bp
DEFINITION	C. annum	PCRTC mRNA.	
VERSION	X80756		
ACCSSION	X80756.1	GI:984112	
WORDS	calreticulin.		
ORIGIN	Capricum annum.		
ORGANISM	Capricum annum		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	euphylliphytes; Spermatophyta; Magnoliophyta; eudicotyledons;		
TITLE	Assteridae; Solananae; Solanales; Solanaceae; Capsicum.		
JOURNAL	1 (bases 1 to 1543)		
MEDLINE	Hugueney,P., Bouvier,F., Badillo,A., d'Harlingue,A., Kuntz,M. and		
REFERENCE	Camara,B.		
AUTHORS	Identification of a plastid protein involved in vesicle fusion		
TITLE	and/or membrane protein translocation		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 92 (12), 5630-5634 (1995)		
FEATURES	95296365		
SOURCE	2 (bases 1 to 1543)		
	Camara,B.		
	Direct Submission		
	Submitted (29-JUL-1994) B. Camara, IBMP CNRS, 12 rue du General		
	Zimmer, 67084 Strasbourg Cedex, FRANCE		
	location/Qualifiers		
	1..1543		
	/organism="Capsicum annum"		
	/db_xref="taxon:4072"		
BASE COUNT	452 a	312 c	376 g
ORIGIN	403 t		

Query Match	28.6%; Score 72.6; DB 7; Length 1543;
Best Local Similarity	59.4%; Pred. NO.1.9e-12;
Matches 117; Conservativity	0; Mismatches 80; Indels 0; Gaps 0;

Oy	57	tcgctcaagcactgtnctttccttcnaactcgcacactctcatctgctgagatcttc	116
Db	1	TCTCTATTCATTCGCTGTTCCTCTACTTGTAGCCTCCGCCGCCCAAATTTTTTC	60
Oy	117	tctgaagagagatctgaagatctgaagagacgcnctgctcncgccatggaagag	176
Db	61	TTTCGAGGAAAATTTCAATGATGCTGCGGAGACACCAATGGGTAATTCATTGCAAGAA	120
Oy	177	agtgagagaaaaggcggtactccttcagacacacagcagaaaaatggtctggagtcngat	236
Db	121	GACGAGAACATGTGGCGGAGAGTGAATCACACCTCTGGCAAGTGGAGTAGACGCTAAT	180
Oy	237	gacmaaggcttcagac	253
Db	181	GACAAAGCTATCCAGAC	197

RESULT 13	AC006932	89479 bp	DNA	PLN	11-OCT-2000
LOCUS	AC006932/c				
DEFINITION	Genomic sequence for Arabidopsis thaliana BAC T27G7 from chromosome				
ACCESSION	I, complete sequence. AC006932				

VERSION	AC006932.8	GI:6468048
KEYWORDS	HTG.	
SOURCE	thale cress.	
ORGANISM	Arabidopsis thaliana	
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.	
AUTHORS	1 (bases 1 to 89479) Shinn,P., Brooks,S., Buehler,E., Chao,Q., Johnson-Hopson,C., Khan,S., Kim,C., Altafi,H., Bel,O., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharasy,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Federspiel,N.A., Theologis,A. and Ecker,J.R.	
TITLE	Genomic sequence for Arabidopsis thaliana BAC T2767 from chromosome I	
JOURNAL	Unpublished	
REFERENCE	2 (bases 1 to 89479) Ecker,J.R.	
AUTHORS	Direct Submission	
TITLE	Submitted (02-MAR-1999) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	
JOURNAL	3 (bases 1 to 89479) Ecker,J.R.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (20-MAY-1999) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	
TITLE	4 (bases 1 to 89479) Ecker,J.R.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (30-OCT-1999) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	
TITLE	5 (bases 1 to 89479) Ecker,J.R.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (25-NOV-1999) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA	
JOURNAL	6 (bases 1 to 89479) Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C., Shinn,P., Altafi,H., Bel,B., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharasy,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.	
REFERENCE	Direct Submission	
AUTHORS	Submitted (03-JAN-2000) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA	
TITLE	7 (bases 1 to 89479) Chao,Q., Brooks,S., Buehler,E., Johnson-Hopson,C., Khan,S., Kim,C., Shinn,P., Altafi,H., Bel,B., Chin,C., Chlou,J., Choi,E., Conn,L., Conway,A., Gonzales,A., Hansen,N., Howing,B., Koo,T., Lam,B., Lee,J., Lenz,C., Li,J., Liu,A., Liu,J., Liu,S., Mukharasy,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J., Southwick,A., Thaveri,A., Toriumi,M., Vaysberg,M., Yu,G., Davis,R., Federspiel,N., Theologis,A. and Ecker,J.	
JOURNAL	Direct Submission	
REFERENCE	Submitted (11-OCT-2000) Arabidopsis thaliana genome center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA	
AUTHORS	On Nov 25, 1999 this sequence version replaced gi:6143825.	
COMMENT	Location/Qualifiers	
FEATURES	1..89479	
SOURCE	/organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1" /clone="T2767"	

VERSION	X89813.1	GI:927571
KEYWORDS	calreticulin; precursor.	
SOURCE	Zea mays.	
ORGANISM	Zea mays.	
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; eumhyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.	
AUTHORS	1 (bases 1 to 1614)	
TITLE	Dresselhaus,T., Hagel,C., Lotz,H. and Kranz,E.	
JOURNAL	Isolation of a full-length cDNA encoding calreticulin from a PCR library of in vitro zygotes of maize	
MEDLINE	Plant Mol. Biol. 31 (1), 23-34 (1996)	
REFERENCE	96309381	
AUTHORS	2 (bases 1 to 1614)	
TITLE	Dresselhaus,T.	
JOURNAL	Direct Submission	
MEDLINE	Submitted (19-JUL-1995) T. Dresselhaus, Applied Plant Molecular Biology II, University of Hamburg, Ohnhorststr. 18, D-22609 Hamburg, FRG	
FEATURES	Location/Qualifiers	
SOURCE	1..1614	
	/organism="Zea mays"	
	/cultivar="Indred Line A188"	
	/db_xref="taxon:4577"	
	/dev_stage="in vitro zygotes, 18h after in vitro fertilisation"	
	/clone_1lb="cDNA library of zygotes"	
	/clone_zmw_233"	
	76..1341	
CDS	/codon_start=1	
	/product="Calreticulin precursor"	
	/protein_id="CA61939.1"	
	/db_xref="GI:927572"	
	/db_xref="SPRMBL:Q43712"	
	/translation="MATIRKGSVAVALALASVAAVAAGEVFEQEKFDGMESRWKS EMKRDNAGEMNHTSGKMNDADAKDGIQTSDFYRAISNEVEPSNRKDTLYQRS VKHEOKLDGGGYKLJAGVDQKKEGDYSIIMFDPDICYSTKRVTHTLTIDGNKN HLIKRDVPCEITDTHVYTLLIRPDATYSILINDEEKOQSIEHMDILPPKTKDPE AKKEDMDKEIVIPDDPKKREGYDJPIKETPDDAKKPEDMDEEDGEWTAPTIIPNP EYKPMKKOKRIKKNYGCKMKAPMINDPFDDPYIYAPOSILAKYIELMOVSGTLF DNITITDDPALAKTFAREETWCKHKAEKAFADEAKKREBDAAKGDDDEDDELDEE DDEKADEKADSDAEDSKSDDEKHDEL"	
	polya_signal 1374..1379	
	polya_signal 1441..1446	
	polya_signal 1495..1500	
	polya_signal 1564..1569	
	polya_site 1596	
BASE COUNT	473 a 343 c 446 g 352 t	
ORIGIN		
Query Match	28.2%	Score 71.6; DB 33; Length 1614;
Best Local Similarity	67.1%;	Pred.No.3.9e-12;
Matches	98; Conservative	0; Mismatches 48; Indels 0; Gaps 0;
Oy	108 gagattctcttcgaagaagatcgaaagtgaagacgcnltgggtgcancgat	167
Db	151 GAGGCTTCTTCACGACAGAAGTTCCGAATGCCTGGCAAAGTAGTGCTCAAGTCTAG	210
Oy	168 tggaaaaggagtgaaagaaacggtactccctcaagcacagcagaagaatagtgctgg	227
Db	211 TGGAGAGAAAGATGAGAACNTGGCTGTGATTGAGAACACACTCGGAAATAATGGAATGA	270
Oy	228 gatcngatgcnaaggtccttacc	253
Db	271 GATGCCGAGGACAAGATTTCACAC	296
RESULT	15	
ZMCRTIGEN	ZMCRTIGEN	1342 bp mRNA PLN 01-NOV-1997
DEFINITION	Zea mays CRT1 gene for calcium-binding protein.	
ACCESSION	Z46772	

	KEYWORDS	Zn6772.1 GI:577611
	KEYWORDS	calcium-binding protein; calreticulin; CRTI gene.
	SOURCE	Zea mays.
	ORGANISM	Zea mays
	REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
	AUTHORS	Poaceae: Zea.
	TITLE	JOURNAL
	AUTHORS	Boyce,J.M. Direct Submission Submitted (21-NOV-1994) Boyce J. M., University of Oxford, Department of Plant Sciences, South Parks Road, Oxford, England,
	FEATURES	Ox1 3A
	source	Location/Qualifiers 1..1342 /organism="Zea mays" /strain="var Merit" /db_xref="taxon:4577" /cisue_type="root tips" /clone_lib="lambda gtl1 (Clontech Cat No: FL1110b)" /gene="" /gene="CRT1" 59..133 59..133 /gene="CRT1" 59..1324 59..1324 /gene="CRT1" /standard_name="calreticulin" /function="calcium sequestration" /citation=[1] /ecodon_start=1 /evidence=experimental /product="calcium-binding protein" /protein_id="CA86728.1" /db_xref="GI:577612" /db_xref="SPRMBL:Q43712" /translotion="MATIRKSSVAALLALASVAAVAGEVFPOEFEDGESHWKS EMKDMMAGMNHTSGKNMGDAADSKITOTSEDRFAISNEVEPSNKDKTLVLQTS VKHQKLDCGGGYWKLGSVDQKKFEGDYSYTFGPDIGYSTKVIVTILTKDNKN HLKRWDPCETDQLTHVTYLIPRDATSYSLIDNBEQTQSIEHMDLIPEAKIKDPRE EKKEPDMDDKEXIPIPEDPKPEGYDIPEKIIPDOAKPEMDEDEGEWTAP11PMNP AYKPWMOKXKITRNPNYGKMKAPMIQNDFEPDOPYIAFDLSLAYIGEIMOVKGSTLE DNIIITPPALAKTFAEFTWGKHKAERKAAPDEAFKKKEBEDAAKGDDEDDELDEEEB DDEKADBDKADSDEDSKSDDEKOHEPL"
	sly_peptide	134..1321
	CDS	/gene="CRT1" /function="calcium sequestration" /evidence=experimental /product="calreticulin" 716..739 /gene="CRT1" 767..800 /gene="CRT1" 821..844 /gene="CRT1"
	repeat_unit	repeat_unit
	BASE COUNT	393 A 287 C 387 G 275 T
	ORIGIN	
	Query Match	27.6%; Score 70; DB 33; Length 1342:
	Best Local Similarity	66.4%: Pred. No. 1,2e+11;
	Matches 97; Conservative	0; Mismatches 49; Indels 0; Gaps 0;
Oy	108	gagattcttcgaagaagatcgcgaagtgaaggacccgnltgggtctancgccgat 167
Dz	134	GAGCTCCTTCACGAGAAGATTCCAGACCGGTGCGAAGACTTAGTGCTCAAGTCTGAG 193
Oy	168	tggaaagagatlgaaaagaaagcggtacccttcaaacacacagcacgaagaaatggtctcgg 227

Mon Mar 19 12:20:51 2001

us-09-199-129a-1.rge

Page 10

Db	194 TGGAAAGGATGTGAACATCTGCTGTGAATTGCACCACACTCTGGGAAAATGGAAATGGA 253
Q7	228 galcngatgacnaagylcttcagaaac 253
Db	254 GATGCCGAGGACAAGAATTTCAAAC 279

Search completed: March 18, 2001, 07:53:46
Job time: 2188 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2001, 07:19:53 ; Search time 73.44 Seconds
(without alignments)
1299.269 Million cell updates/sec

Title: US-09-199-129A-1
Perfect score: 254
Sequence: 1 ggaatcagagctaccta.....atgacnaagcttcagaca 254

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 480022 seqs, 187831343 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
N.Geneseq_36: *
1: /cgn2_2/gcgdata/geneseq/geneseqn/NA1980.DAT: *
2: /cgn2_2/gcgdata/geneseq/geneseqn/NA1981.DAT: *
3: /cgn2_2/gcgdata/geneseq/geneseqn/NA1982.DAT: *
4: /cgn2_2/gcgdata/geneseq/geneseqn/NA1983.DAT: *
5: /cgn2_2/gcgdata/geneseq/geneseqn/NA1984.DAT: *
6: /cgn2_2/gcgdata/geneseq/geneseqn/NA1985.DAT: *
7: /cgn2_2/gcgdata/geneseq/geneseqn/NA1986.DAT: *
8: /cgn2_2/gcgdata/geneseq/geneseqn/NA1987.DAT: *
9: /cgn2_2/gcgdata/geneseq/geneseqn/NA1988.DAT: *
10: /cgn2_2/gcgdata/geneseq/geneseqn/NA1989.DAT: *
11: /cgn2_2/gcgdata/geneseq/geneseqn/NA1990.DAT: *
12: /cgn2_2/gcgdata/geneseq/geneseqn/NA1991.DAT: *
13: /cgn2_2/gcgdata/geneseq/geneseqn/NA1992.DAT: *
14: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT: *
15: /cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT: *
16: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT: *
17: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT: *
18: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT: *
19: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT: *
20: /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT: *
21: /cgn2_2/gcgdata/geneseq/geneseqn/NA2000.DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30.8	12.1	2518	20	V71745 Human V3 loop HIV
2	30.2	11.9	10942	20	V71742 Human V3 loop HIV
3	29.8	11.7	1230025	20	X91990 Nucleotide sequence
4	28.4	11.6	1361	20	X16671 G-protein coupled
5	29.2	11.5	3046	19	V29074 Rattus norvegicus
6	29	11.4	401	14	O60805 Human brain Express
7	28.6	11.3	250	20	X40841 Human secreted pro
8	28.6	11.3	323	20	X40452 Human secreted pro
9	28.6	11.3	2168	20	X52271 Protein PRO330 CDN
10	28.4	11.2	251	20	V90169 EST clone DF706.
11	28.4	11.2	2082	15	O55789 Sequence comparsin
12	28.4	11.2	2382	12	O10238 Encodes membrane e

C 13	28.2	11.1	3525	20	X91788 Porphyromonas ging
C 14	28.2	11.1	3696	20	X91787 Porphyromonas ging
C 15	28.2	11.1	3798	20	X91786 Porphyromonas ging
C 16	28.2	11.1	3807	20	X91646 Porphyromonas ging
C 17	28.2	11.1	4789	20	X80992 Human steroid rece
C 18	28.2	11.1	6835	20	V99915 AIB1 (Amplified in
C 19	28	11.0	1819	16	V74981 Staphylococcus aur
C 20	28	11.0	3303	16	O76024 TGF-beta-3 promote
C 21	28	11.0	5355	20	X89220 Seq ID No: 28 of W
C 22	28	11.0	5355	20	X89221 Seq ID No: 30 of W
C 23	28	11.0	5355	21	Z39404 Human T1ad protein
C 24	28	11.0	5355	21	Z39405 Human T1ad protein
C 25	28	11.0	6395	16	O95155 Tobacco mosaic vir
C 26	28	11.0	6395	20	Z20642 TMV-based virus TM
C 27	28	11.0	6439	20	Z20644 TMV-based virus TM
C 28	28	11.0	6439	20	Z20643 TMV-based virus TM
C 29	28	11.0	6446	20	Z20645 TMV-based virus TM
C 30	28	11.0	6475	20	Z20646 TMV-based virus TM
C 31	28	11.0	7926	21	X89190 Plasmid T701A 103L
C 32	27.6	10.9	1353	20	X91657 Porphyromonas ging
C 33	27.6	10.9	1362	20	X91536 Porphyromonas ging
C 34	27.6	10.9	2005	20	X77849 Ribozyme PBPI3817
C 35	27.6	10.9	2874	20	X77838 HIV2 strain val3
C 36	27.6	10.9	2975	20	X77837 HIV2 strain Mar6 3
C 37	27.6	10.9	3986	14	O46263 NF-1 CDNA gene seq
C 38	27.6	10.9	4549	17	V74485 Staphylococcus aur
C 39	27.6	10.9	8937	13	O20602 NF1 gene. Homo sa
C 40	27.6	10.9	9319	21	A34873 Human adenosine re
C 41	27.6	10.9	10706	18	T46941 Human neurofibroma
C 42	27.6	10.9	1664976	19	V21209 Methanococcus jann
C 43	27.4	10.8	43676	21	Z60606 Nucleotide sequenc
C 44	27.2	10.7	1679	21	Z48767 Human C1PR coding
C 45	27	10.6	19718	19	V52232 Streptococcus pneu

ALIGNMENTS

RESULT 1	
ID V71745	standard; CDNA: 2518 BP.
XX	
AC V71745:	
XX	
DT 15-MAR-1999	(first entry)
XX	
DE Human V3 loop HIV receptor P95/nucleolin CDNA.	
XX	
KW HIV receptor; V3 loop; human immunodeficiency virus; retrovirus;	
KW P95 protein; nucleolin; infection; therapy; diagnosis; ss.	
XX	
OS Homo sapiens.	
XX	
FH Key	Location/Qualifiers
FT CDS	112..2235
FT	/*tag= a
XX	
PN WO98040480-A1.	
XX	
PD 17-SEP-1998.	
XX	
PF 12-MAR-1998;	98WO-EP01409.
XX	
PR 12-MAR-1997;	97US-0040969.
XX	
PA (CNRS) CENT NAT RECH SCI.	
XX	
PA (INSP) INST PASTEUR.	
XX	
PI Briand J, Callebaut C, Guichard G, Hovassessian A;	
XX	
PI Jacotot E, Krust B, Muller S;	
XX	
DR WPI: 1999-034588/03.	
DR P-PSDB: W84052.	

PN MO9840480-A1.
 XX
 PD 17-SEP-1998.
 XX
 PF 12-MAR-1998; 98MO-EP01409.
 XX
 PR 12-MAR-1997; 97US-0040969.
 XX
 PA (CNRS) CENT NAT RECH SCL.
 PA (INSP) INST PASTEUR.
 XX
 PI Briand J, Callebaut C, Guichard G, Hovanessian A;
 PI Jacotot E, Krust B, Muller S;
 XX
 DR WPI: 1999-034588/03.
 DR P-PSDB: W84052.
 XX
 PY New isolated V3 loop HIV receptor - comprises p95/nucleolin,
 PT P40/PHAPI and p30/PHAPI proteins, used to develop products for the
 PT treatment and prevention of HIV infection
 XX
 Claim 17, Fig 49(1-10); 267pp; English.
 XX
 CC This genomic DNA codes for the p95 (or nucleolin) protein of the
 CC newly identified V3 loop HIV receptor. This novel protein complex
 CC receptor for HIV retroviruses consists of an association of 3
 CC proteins named p95/nucleolin, p40/PHAPI and p30/PHAPI (see
 CC W84052-54). These proteins were isolated from human CD4+ CEM
 CC T-cell extracts using an affinity matrix containing either the
 CC pseudopeptide 5(KPSICH2)NPK-template assembled synthetic peptide
 CC or a synthetic V3 loop peptide (see W84055). p95 was identified
 CC as nucleolin by amino acid sequence analysis. The invention also
 CC concerns peptidic or non-peptidic molecules having the ability to
 CC alter and/or prevent the binding of the novel HIV receptor to the
 CC HIV retrovirus, and to pharmaceutical and diagnostic compositions
 CC containing such molecules. Methods are provided for screening for
 CC new active molecules, and to methods of screening genetic defects
 CC in the expression of the V3 loop HIV receptor in individuals that
 CC survive long-term HIV infection or who are HIV-resistant. Such
 CC genetically defective polynucleotides can be used in gene therapy.
 XX
 SQ Sequence 10942 BP: 2873 A; 2245 C; 2723 G; 3101 T; 0 other;
 XX

PN		M09927105-A2.	
XX			
PD		03-JUN-1999.	
XX			
Pf		20-NOV-1998;	98WO-IBO1890.
XX			
PR		04-NOV-1998;	98US-0107078.
XX		21-NOV-1997;	97FR-0014673.
PA	(GEST) GENSET.		
XX			
PI	Griffais R;		
XX			
DR		WPI: 1999-357842/30.	
PT			
XX			
PS	Genome sequence of Chlamydia pneumoniae		
XX			
PS	Claim 1; Page 291-611; 1912pp; English.		
CC	The present sequence represents the complete genome of Chlamydia		
CC	pneumoniae, and encodes proteins YJ4584-YJ5879. C. pneumoniae causes		
CC	respiratory disease such as pneumonia and bronchitis and is thought		
CC	to have a contributing factor in heart disease, sarcoidosis, sinusitis,		
CC	purulent otitis media, erythema nodosum or pharyngitis. The polypeptides		
CC	encoded by the open reading frames of the C. pneumoniae genome (see		
CC	YJ4584-YJ5879) can be used in immunogenic compositions as vaccines.		
CC	Vectors containing C. pneumoniae nucleotide sequences can also be		
CC	used as immunogenic compositions, especially where the vector directs		
CC	the expression of a neutralising epitope of C. pneumoniae.		
SO	Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other:		
	Query Match	11.7%; Score 29.8; DB 20; Length 1230025;	
	Best Local Similarity	50.8%; Pred. No. 27;	
	Matches , 61; Conservative 0; Mismatches 59; Indels 0; Gaps 0;		
Oy	18 ttaaggaataatgnaattggccaanncgcagaacactagtcagtctcaagctacttgnct 77 Db 1207734 TTAAAGGAAGAAMTACATTACCCAAGCTCATGGCGATAGAAATCGTTGGAGGTACTAAGGGTCr 12076753		
Oy	78 ttccctcnaactctcgacctcttcattcgtctgtagattttcttcgaagaagagattcgaagat 137 Db 1207674 CGGCTTGTCACAGGCACCTGCCAACCTCCTGTGACGGTAGAAGAACAACCTAGCCGCTTAT 1207615		
RESULT	4		
XI6671/C	XI6671 standard; cDNA; 1361 BP.		
XX			
AC	XI6671;		
XX			
Df	29-APR-1999 (first entry)		
DE	G-protein coupled receptor HM74A encoding cDNA.		
XX			
KM	HM74A receptor; G-protein coupled receptor; infection; pain; cancer; diabetes; obesity; neurological disorder; heart failure; hypertension; asthma; allergy; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Oualifiers	
FT	CDS	61..1152	
FT	'	/**rag-a	
FT		/product= "HM74A receptor"	
XX			
PN	M09856820-A1.		
XX			
PD	17-DEC-1998.		
PF			
XX	12-JUN-1998;	98WO-US12386.	
XX			

PR 12-JUN-1997; 97US-0049480.
XX (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Elshourbagy NA, Guerrero SF, Li X, Mooney JL;
XX WPI: 1999-095273/08.
DR P-PSDB: M94654.
XX
XX New isolated G-protein coupled receptor, HM74A - used to develop
PT products for treating e.g. infections, pain, cancers, diabetes,
PT obesity, neurological disorders, heart failure, hypertension, asthma
PT or allergies
XX
PS Claim 2; Page 30-31; 40pp; English.
XX
XX The present sequence encodes a member of the G-protein coupled receptor
CC (77m receptor) family, designated the HM74A receptor. The proteins,
CC agonists, antagonists and polynucleotides can be used for treating
CC disorders associated with increased or reduced expression or activity
CC of HM74A, e.g. bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by HIV-1 or HIV-2, pain, cancers,
CC diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease,
CC acute heart failure, hypotension, hypertension, urinary retention,
CC osteoporosis, angina pectoris, myocardial infarction, stroke, ulcers,
CC asthma, allergies, benign prostatic hypertrophy, migraine, vomiting,
CC psychotic and neurological disorders, including anxiety, schizophrenia,
CC manic depression, depression, delirium, dementia, and severe mental
CC retardation, and dyskinesias such as Huntington's disease or
CC Gilles de la Tourette's syndrome. The products can also be used for
CC detection, diagnosis and drug screening.
XX
SQ Sequence 1361 BP; 291 A; 390 C; 342 G; 338 T; 0 other;
Query Match 11.6%; Score 29.4; DB 20; Length 1361;
Best Local Similarity 57.3%; Pred. No. 1.8;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
QY 96 tcttcattcgctgatttcttcgaagagagatcgagaatggaagagccnctg 155
DB 553 TCTTCAGGAGGTGACGTCTCAGGCCAATGATGCCCCACGAAAGCAGATGATGG 494
QY 156 gtgtcancgcattggaagaagatgaagg 184
DB 493 CTGCTGCCATGAGATCTTGTTCACG 465
XX
XX 5
XX 11-SEP-1998 (first entry)
XX Rattus norvegicus NRL gene 5' region.
XX DE Rattus norvegicus NRL gene 5' region.
XX KM 5' region; NRL gene; neu-related lipocalin; promoter; therapy;
XX study; breast cancer; mammary gland; ds.
XX OS Rattus norvegicus.
XX
XX Key Location/Qualifiers
XX FT promoter 1154..2967
XX FT /*tag= a
XX FT misc_feature 2967
XX FT /*tag= b
XX FT /*note= "putative transcription start site"
XX FT TATA_signal 2939..2945
XX FT /*tag= c
XX PN M09815634-A1.

XX
PD 16-APR-1998.
XX
XX 05-MAY-1997; 97WO-US07504.
XX
XX 07-OCT-1996; 96US-0726725.
XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Chen K, Gould MN;
XX WPI: 1998-240820/21.
XX
XX New isolated mammary gland specific promoters - can be used to
PT promote gene expression in the mammary gland in a constant manner
PT throughout the estrous cycle
XX
PS Disclosure: Fig 2; 48pp; English.
XX
XX The sequence is that of the 5' region of the rat NRL
CC (neu-related lipocalin) gene. The sequence contains a mammary
CC gland-specific promoter which can be used for targeting foreign gene
CC expression to the mammary gland. It can be used in therapy and study
CC of e.g. breast cancer genes.
XX
SQ Sequence 3046 BP; 727 A; 723 C; 857 G; 739 T; 0 other;
Query Match 11.5%; Score 29.2; DB 19; Length 3046;
Best Local Similarity 50.0%; Pred. No. 3;
Matches 67; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 66 gctactgnccttcttcctcnaactcgcactcttcactcgtcgagatttctcgaag 125
DB 1964 gatgccttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctg 2023
QY 126 agatcgaagatgagtggaagagccnctggtgtcancgcattggaagaagatgaaga 185
DB 2024 ttcttcgagctggtggaacaaaccagggagatgcttcttcgaaggagataactaaga 2083
QY 186 aaagcgggtacct 199
DB 2084 gaagtggaacct 2097
XX
XX RESULT 6
XX Q60805/c
XX ID Q60805 standard; DNA: 401 BP.
XX AC Q60805;
XX
XX 16-MAR-1994 (first entry)
XX DE Human brain Expressed Sequence Tag EST00911.
XX KM Gene transcription product; genetic markers; tagging; in vivo;
XX transcription; mapping; locations; chromosomes; chromosomal; ss.
XX OS Homo sapiens.
XX PN M09316178-A.
XX
XX 19-AUG-1993.
XX PD
XX 12-FEB-1993; 93WO-US01294.
XX PF
XX 12-FEB-1992; 92US-0837195.
XX PR
XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
XX PA Adams MD, Moreno RF, Venter CJ;
XX PI
XX WPI: 1993-272882/34.
XX DR

XX Enriched oligonucleotides and corresp. sequences - used as
PT markers for human genes transcribed in-vivo, facilitate tagging
PT of most human genes
XX
PS Example 4; Page 393; 500pp; English.
XX
XX The Expressed Sequence Tag was isolated from a human brain cDNA
CC library as part of a large set of ESTs which can be used as markers
CC for human genes transcribed in vivo. They can be used to facilitate
CC tagging of most human genes, for mapping locations of expressed genes
CC on chromosomes, for individual or forensic identification, for mapping
CC locations of disease-associated genes, for identification of tissue
CC type, and for prep. of antisense sequences, probes and constructs.
CC EST00911 has a "poor" coding probability as evaluated using the
CC coding-region prediction program CRM. See also Q59041-Q61440.
XX
SQ Sequence 401 BP; 139 A; 69 C; 64 G; 128 T; 1 other:

Query Match 11.4%; Score 29; DB 14; Length 401;
Best Local Similarity 47.3%; Pred. No. 1.4;
Matches 71; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

OY 25 aaatgnanalgccaanngcaacactagtcgctccaagctacttgncttccctc 84
DB 384 AAAGTAAATTCCTATCTGATTTATCTGATTCATTCATGTCANGTCAATGAATATTTTA 325
OY 85 naactctgacctcttcattcgcgcgagatttcttcgaagagagatccgaagatgatgga 144
DB 324 CCACATGACACCTATTAATAATCTCTAGATATTTTTCAGAAAGAAATTAACCATGGT 265
OY 145 agagccgcgtggtcancgcagattgga 174
DB 264 ATATTGTTACTTCTCTCATCTGCAAAA 235

RESULT 7
X40841
ID X40841 standard; cDNA; 250 BP.
XX
AC X40841;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO: 53.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KM forensic; gene therapy; chromosome mapping; signal peptide;
KM upstream regulatory sequence; cytokine activity; cell proliferation;
KM differentiation; haematopoiesis regulation; tissue growth regulation;
KM reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KM thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
XX Homo sapiens.
OS
PN WO906554-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-1B01238.
XX
PR 01-AUG-1997; 97US-0905134.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI; 1999-153784/13.
XX
DR P-PSDB; Y12008.
XX
PT New nucleic acids encoding human secreted proteins - obtained from
PT cDNA libraries prepared from kidney, fetal kidney, dystrophic

PT muscle, muscle and heart tissue
XX
XX Claim 1; Page 184-185; 622pp; English.
XX
XX X40826 to X41093 represent 5' expressed sequence tags (ESTs) for human
CC secreted proteins, and encode the proteins given in Y01602 and
CC Y11994 to Y12260, respectively. The proteins given represent the signal
CC peptide and an N-terminal fragment of a secreted protein. The nucleic
CC acid sequences can be used for producing secreted human gene products.
CC They can also be used to develop products for diagnosis and therapy.
CC The proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding the signal peptide can be used
CC for directing extracellular secretion of a polypeptide or the insertion
CC of a polypeptide into a membrane, or importing a polypeptide into
CC a cell.
XX
SQ Sequence 250 BP; 55 A; 61 C; 78 G; 53 T; 3 other:

Query Match 11.3%; Score 28.6; DB 20; Length 250;
Best Local Similarity 59.7%; Pred. No. 1.5;
Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

OY 137 tggatgtgaagccgnltggtctgctancgcattgaaagagtgaaagaaacggtac 196
DB 83 tgcagaaaccgcaagcagtgcttaaccagtgagacagcgcatgtgaagagcggtgaag 142
OY 197 cttcaagcaacacagcag 213
DB 143 gtccctgcccagagcag 159

RESULT 8
X40452
ID X40452 standard; cDNA; 323 BP.
XX
AC X40452;
XX
DT 18-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO: 52.
XX
XX Human; secreted protein; EST; expressed sequence tag; diagnosis;
KM forensic; gene therapy; chromosome mapping; signal peptide; prostate;
KM upstream regulatory sequence; cytokine activity; cell proliferation;
KM differentiation; haematopoiesis regulation; tissue growth regulation;
KM reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KM thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
XX Homo sapiens.
OS
PN WO906550-A2.
XX
PD 11-FEB-1999.
XX
PF 31-JUL-1998; 98WO-1B01232.
XX
PR 01-AUG-1997; 97US-0905144.
XX
PA (GEST) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI; 1999-153780/13.
XX
DR P-PSDB; Y11730.
XX

CC particular isotype. The extracellular segment forms an epitope
CC unique to the B cells which produce each isotype. These membrane
CC bound immunoglobulin isotype-specific extracellular epitopes are
CC not present on the secreted, soluble form of the immunoglobulins.
XX
SQ Sequence 2082 BP; 491 A; 459 C; 712 G; 399 T; 21 other;

Query Match 11.2%; Score 28.4; DB 15; Length 2082;
Best Local Similarity 55.2%; Pred. No. 4.7;
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 132 gaagatgatgaagagagccnltggtgctanccgattgaaagagtgaaagaaacg 191
||| ||||| ||||| ||| ||| ||| ||||| ||| ||||| ||| ||||| |||
Db 752 gatgagagatggaaggggtggatggaatggaatggaatggaatggaatggaatg 811
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 gttacctcaagcacagcagcaaaatggtcgtg 227
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 gttgactgacgagagattgagatcctgggttgg 847

RESULT 12

ID Q10238 standard; cDNA; 2382 BP.

AC Q10238;

DT 22-MAR-1991 (first entry)

DE Encodes membrane exon of IGA membrane anchoring peptide.

KW alpha.mb/ec; immunoglobulin A; IGA; allergy; membrane-anchoring;
peptide; ss.

XX Homo sapiens.

OS Location/Qualifiers

FT Key 1741..1956

FT exon

FT /tag= a

FT /product= alpha.mb/ec

FT /note= "membrane-anchoring peptide"

FT polyA_signal 2361..2366

FT /tag= b

XX MO9015614-A.

XX PD 27-DEC-1990.

XX F 21-JUN-1990; 90WO-US03532.

XX PR 22-DEC-1989; 89US-0455080.

XX PR 21-JUN-1989; 89US-0369479.

XX PA (TANO-) TANOX BIOSYST INC.

XX PI Chang TW, Chang NT;

XX DR WPI: 1991-022051/03.

XX DR R-PSDB: R10202.

XX PT Antibody prep. which binds specifically to immunoglobulin-A -

XX PT bound to B cells, but not secreted form, to enhance Iga prodn.

XX PT and protect against allergy and infection

XX PS Disclosure: Fig 1; 54pp; English.

XX Clones containing alpha 1 heavy chain gene segments were identified
CC from a human genomic library, subcloned and sequenced. A segment of
CC 14 nucleotides was determined to be the membrane exon of the alpha
CC gene. To confirm this, total RNA was isolated from a human mlgA-
CC expressing cell line DAKKI and cDNA prepared from it. Positive
CC clones were sequenced and two species of human membrane-bound alpha1
CC mRNA were found, resulting from two different splice sites and

CC encoding two isoforms. Isoform 2 is the one corresponding to R10202;
CC isoform 1 lacks the first 6 N-terminal amino acids. The nucleotide
CC sequence of human alpha1 is homologous to that of murine alpha.
XX
SQ Sequence 2382 BP; 555 A; 549 C; 809 G; 469 T; 0 other;

Query Match 11.2%; Score 28.4; DB 12; Length 2382;
Best Local Similarity 55.2%; Pred. No. 5;
Matches 53; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 132 gaagatgatgaagagagccnltggtgctanccgattgaaagagtgaaagaaacg 191
||| ||||| ||||| ||| ||| ||| ||||| ||| ||||| ||| ||||| |||
Db 752 gatgagagatggaaggggtggatggaatggaatggaatggaatggaatggaatg 811
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 192 gttacctcaagcacagcagcaaaatggtcgtg 227
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 812 gttgactgacgagagattgagatcctgggttgg 847

RESULT 13

ID X91788/c standard; DNA; 3525 BP.

AC X91788;

DT 25-AUG-1999 (first entry)

DE Porphyromonas gingivalis protein PG9 encoding DNA.

KW Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
vaccine; antigenic; ds.

XX Porphyromonas gingivalis.

XX OS WO9929870-A1.

XX PD 17-JUN-1999.

XX PF 10-DEC-1998; 98WO-AU01023.

XX PR 04-AUG-1998; 98AU-0005028.

XX PR 10-DEC-1997; 97AU-0000838.

XX PR 31-DEC-1997; 97AU-0001182.

XX PR 30-JAN-1998; 98AU-0001546.

XX PR 10-MAR-1998; 98AU-0002264.

XX PR 09-APR-1998; 98AU-0002911.

XX PR 23-APR-1998; 98AU-0003128.

XX PR 05-MAY-1998; 98AU-0003338.

XX PR 22-MAY-1998; 98AU-0003654.

XX PR 29-JUL-1998; 98AU-0004917.

XX PA (CSLC-) CSL LTD.

XX PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;

XX PI Ross BC, Rochel LJ, Webb EA;

XX DR WPI: 1999-385613/32.

XX DR P-PSDB: Y34570.

XX FT Antigenic Porphyromonas gingivalis peptides for preventing

XX FT gingivitis

XX PS Claim 12; Page 268; 588pp; English.

XX X91536 to X91801 encode two hundred and sixty six antigenic
CC Porphyromonas gingivalis (PG) polypeptide sequences given in Y24318 to
CC Y34583. X91802 to X91989 represent PCR primers used in the isolation
CC of the PG polypeptides. The PG polypeptides have antibacterial activity
CC with a vaccine mechanism of action. The PG polypeptides can be used as
CC vaccines especially against Porphyromonas gingivalis. Probes can be
CC used to detect Porphyromonas gingivalis in standard hybridisation assays.
CC Porphyromonas gingivalis is involved in periodontal disease especially

CC gingivitis.
XX
SQ Sequence 3525 BP; 1115 A; 738 C; 777 G; 895 T; 0 other;

Query Match 11.1%; Score 28.2; DB 20: Length 3525;
Best local Similarity 57.8%; Pred. No. 7.1;
Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps

OY 88 ctctgcacitcattccgcatgaatlttcctcgagaagagatcgaagtgtgatgaaga 147
 ||| | | | | | | | | | | | | | | | | | | | | | | |
DB 1683 CTCGTGCGTGCTCCTGGCATACAGGATTTCTGCCAACAGGACTACACAGATTGCAGGCATA 1624

OY 148 gccgnntgggtgccancgacttg 170
 | | | | | | | | | | | | | | | | | | | | | | | |
DB 1623 GCCTATCTCTCTCAACCACAATACG 1601

RESULT 14
X01787/c
X91787 standard; DNA; 3696 BP.

AC X91787;
DT 25-AUG-1999 (first entry)
DE Porphyromonas gingivalis protein PG9 encoding DNA.
KM Porphyromonas gingivalis; PG, periodontal disease; gingivitis;
KN vaccine; antigenic; ds.
OS Porphyromonas gingivalis.
PN W09929870-Al.
PX
PD 17-JUN-1999.
PE 10-DEC-1998; 98WC-AU01023.
PF
PR 04-AUG-1998; 98AV-0005028.
PR 10-DEC-1997; 97AU-0000839.
PR 31-DEC-1997; 97NU-0001182.
PR 30-JAN-1998; 98AU-0001546.
PR 10-MAR-1998; 98AU-0002264.
PR 09-APR-1998; 98AU-0002911.
PR 23-APR-1998; 98AU-0003128.
PR 05-MAY-1998; 98AU-0003338.
PR 22-MAY-1998; 98AU-0003654.
PR 29-JUL-1998; 98AU-0004917.
PA (CSLC-) CSL LTD.
PI Agius CF, Barr IG, Hocking DM, Margets MB, Patterson MA;
PI Ross BC, Rothel LJ, Webb EA;
XX MPI: 1999-385613/32.
XX P-PSDB: Y34569.
DR
PT Antigenic Porphyromonas gingivalis peptides for preventing
PT gingivitis
PS Claim 12; Page 266-267; 588pp; English.
XX
XX X91536 to X91801 encode two hundred and sixty six antigenic
XX Porphyromonas gingivalis (PG) polypeptide sequences given in Y34318 to
XX Y34393. X91802 to X91899 represent PCR primers used in the isolation
XX of the PG polypeptides. The PG polypeptides have antibacterial activity
XX with a vaccine mechanism of action. The PG polypeptides can be used as
XX vaccines especially against Porphyromonas gingivalis. Probes can be
XX used to detect Porphyromonas gingivalis in standard hybridisation assays.
XX Porphyromonas gingivalis is involved in periodontal disease especially
XX gingivitis.
XX

SQ Sequence 3696 BP: 1171 A; 774 C; 814 G; 937 T; 0 other;
 Query Match 11.1%; Score 28.2; DB 20; Length 3696;
 Best Local Similarity 57.8%; Pred. No. 7.2;
 Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0
 QY 88 ccttcgacatcctcatcgtcgtcgaatttcttcgaagagatcgaagatgaltggaaga 147
 Db 1854 Cgtgtggtgtgtccttccatcaggaatttctccacgacacatgacattgcagcaca 1795
 QY 148 gccagttggagtgctcaccagattg 170
 Db 1794 GGCATCTGTCTCCTAACCATATAG 1772
 RESULT 15
 X91786/c
 ID X91786 standard; DNA; 3798 BP.
 AC X91786;
 DT 25-AUG-1999 (first entry)
 DE Porphyromonas gingivalis protein PG9 encoding DNA.
 KM Porphyromonas gingivalis; PG; periodontal disease; gingivitis;
 KW vaccine; antigenic; ds.
 XX Porphyromonas gingivalis.
 OS
 PN MO9929870-A1.
 PD 17-JUN-1999.
 PF 10-DEC-1998; 98WO-AU01023.
 PR 04-AUG-1998; 98AU-0005028.
 PR 10-DEC-1997; 97AU-0000839.
 PR 31-DEC-1997; 97AU-0001182.
 PR 30-JAN-1998; 98AU-0001546.
 PR 10-MAR-1998; 98AU-0002264.
 PR 09-APR-1998; 98AU-0002911.
 PR 23-APR-1998; 98AU-0003128.
 PR 05-MAY-1998; 98AU-0003338.
 PR 22-MAY-1998; 98AU-0003654.
 PR 29-JUL-1998; 98AU-0004917.
 PA (CSLC-) CSL LTD.
 PI Agius CT, Barr IG, Hocking DM, Margetts MB, Patterson MA;
 PI Ross BC, Roedel LJ, Webb EA;
 DR WPI: 1999-385613/32.
 DR P-PSDB: Y34568.
 XX Antigenic Porphyromonas gingivalis peptides for preventing
 PT gingivitis
 Claim 12; Page 265-266; 588pp; English.
 XX X91536 to X91801 encode two hundred and sixty six antigenic
 CC Porphyromonas gingivalis (PG) polypeptide sequences given in Y34318 to
 CC Y34583. X91802 to X91988 represent PCR primers used in the isolation
 CC of the PG polypeptides. The PG polypeptides have antibacterial activity
 CC with a vaccine mechanism of action. The PG polypeptides can be used as
 CC vaccines especially against Porphyromonas gingivalis. Probes can be
 CC used to detect Porphyromonas gingivalis in standard hybridisation assays.
 CC Porphyromonas gingivalis is involved in periodontal disease especially
 CC gingivitis.
 XX
 Sequence 3798 BP: 1195 A; 792 C; 835 G; 976 T; 0 other;

Query Match 11.18; Score 28.2; DB 20; Length 3798;
 Best Local Similarity 57.8%; Pred. No. 7.3;
 Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
 QY 88 ctctgcactcttcattcgcttgagattttcttcgaagagagattcgaagatgtagtgaaga 147
 DB 1956 CTGTGGTGTCTCTTGGCATTTCCTTCCACAGGACATACACAGATTGACAGCATA 1897
 QY 148 gccgntggtgtctancecgattcg 170
 DB 1896 GGCTATCTGTCTTAACCAATAG 1874

Search completed: March 18, 2001, 07:56:41
 Job time: 2208 sec